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| PR | 19-MAY-1999; | 990US-0134941P. | PR | 28-JUL-1999; | 990US-0145951P. |
| PR | 21-MAY-1999; | 990US-0135353P. | PR | 02-AUG-1999; | 990US-0146386P. |
| PR | 24-MAY-1999; | 990US-0135629P. | PR | 02-AUG-1999; | 990US-0146388P. |
| PR | 25-MAY-1999; | 990US-0136021P. | PR | 02-AUG-1999; | 990US-0146389P. |
| PR | 27-MAY-1999; | 990US-0136322P. | PR | 03-AUG-1999; | 990US-0147038P. |
| PR | 28-MAY-1999; | 990US-0136782P. | PR | 04-AUG-1999; | 990US-0147040P. |
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| PR | 23-JUL-1999; | 990US-0145145P. | PR | 14-OCT-1999; | 990US-0159329P. |
| PR | 23-JUL-1999; | 990US-0145218P. | PR | 14-OCT-1999; | 990US-0159330P. |
| PR | 23-JUL-1999; | 990US-0145224P. | PR | 21-OCT-1999; | 990US-0160767P. |
| PR | 23-JUL-1999; | 990US-0160989P. | PR | 21-OCT-1999; | 990US-0160768P. |
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| PR | 22-OCT-1999; | 990US-0160809P. | PR | 22-OCT-1999; | 990US-0160981P. |
| PR | 22-OCT-1999; | 990US-0160989P. | PR | 22-OCT-1999; | 990US-0160989P. |

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| PR | 25-OCT-1999; | 99US-0163404P. | Db | 841 AATTCGTCACTGCACATTGTGTGACAGAGAAGAAAACCCAAAGCACTGTCAG | 900 |
| PR | 25-OCT-1999; | 99US-0163406P. | QY | 956 AAGGGAAAGCAAGGAGAGCTAGACAGATGCTCAGCGGTATGATTCCGAA | 1015 |
| PR | 26-OCT-1999; | 99US-0163359P. | Db | 901 AAGGGAAAGCAAGGAGAGCTAGACAGATGCTCAGCGGTATGATTCCGAA | 960 |
| PR | 26-OCT-1999; | 99US-0163360P. | QY | 1016 GGCAACAAGTATGCTCTGACGACAAGGGATTAGAACAGAGCTACGACITGCGA | 1075 |
| PR | 26-OCT-1999; | 99US-0163361P. | Db | 961 GGCAGAAAGTATGCTCTGACGACAAGGGATTAGAACAGAGCTACGACITGCGA | 1020 |
| PR | 28-OCT-1999; | 99US-0163920P. | QY | 1076 GCAAGAGAAAGCTGTACCAAAAGCAAGAGAATGACAAGGAATTCAAAGGAA | 1135 |
| PR | 28-OCT-1999; | 99US-0163922P. | Db | 1021 GCAAGAGAAAGCTGTACCAAAAGCAAGAGAATGACAAGGAATTCAAAGGAA | 1080 |
| PR | 29-OCT-1999; | 99US-0162142P. | QY | 1136 AGATGAGGGGGCTACTCAAGAGCCTTTTGTTGATAGTGTATGGCATGGT | 1195 |
| Best Local Similarity | 94.1%; | Score 1195.6; DB 3; Length 1349; | Matches | 1209; Conservative 0; Mismatches 4; Indels 1; Gaps 1; | |
| Matches | 1209; | | Db | 1081 AGATGAGGGGGCTACTCAAGAGCCTTTTGTTGATAGTGTATGGCATGGT | 1140 |
| Conservative | 0; | | QY | 1196 TGTTCCCTTTCTCCGATCTTCGACGCCACAGGTTAAGCAAGTAATGTTGAA | 1255 |
| Mismatches | 4; | | Db | 1141 TGTTCCCTTTCTCCGATCTTCGACGCCACAGGTTAAGCAAGTAATGTTGAA | 1200 |
| Indels | 1; | | QY | 1256 GAAGGTTAACATT 1269 | |
| Gaps | 1; | | Db | 1201 GAAGGTTAACATT 1214 | |
| Db | 181 GGCATCTAAGAGGTTAATGTTCTCTTAAGTTGATGTGAGCTGAGCTGATGAA | 295 | RESULT 2 | | |
| QY | 296 GAAACTCACTGAGAGATTAAAGGAAAGTCACGGTCCAAACCATCCAGTACTCTAC | 355 | ID | AAC61130 | |
| Db | 241 GAAAGTCACTGAGAGATTAAAGGAAAGTCACGGTCCAAACCATCCAGTACTCTAC | 300 | ID | AAC61130 standard; DNA; 1317 BP. | |
| QY | 356 ATGCTTTCTCACTCACAGGCAATTAAAGGAAAGTCACGGTCCAAACCATCCAGTACTCTAC | 415 | XX | | |
| Db | 301 ATGCTTTCTCACTCACAGGCAATTAAAGGAAAGTCACGGTCCAAACCATCCAGTACTCTAC | 360 | XX | | |
| QY | 416 GCATGAGCAACCTTATGTTGAACTGGCTCTGGAAAGAGAAAGAACTAGCGGTT | 475 | DT | Arabidopsis thaliana DNA fragment SEQ ID NO: 49012. | |
| Db | 361 GCATGAGCAACCTTATGTTGTTCTGGAAAGGAAAGAACTAGCGGTT | 420 | XX | | |
| QY | 476 AGCCATCGGGTTGCTGAGCTGCTGGAAAGTGGCTCTGGCTGAA 535 | | XX | | |
| Db | 421 AGCCATCGGGTTGCTGAGCTGCTGGCTCTGGCTGAA 480 | | XX | | |
| QY | 536 ATTACCTTATGGAAAGAGAAACTTTTTCACCTTGTACCTTGGAGCTT | 595 | XX | | |
| Db | 481 ATTACCTTATGGAAAGAGAAACTTTTTCACCTTGTACCTTGGAGCTT | 540 | XX | | |
| QY | 596 GTTATGAGGTGGAGTTTGGTTGATGAAACAAGGAGGAAGCTCGAGTA | 655 | PR | 25-FEB-1999; 99US-0121825P. | |
| Db | 541 GTTATGAGGTGGAGTTTGGTTGATGAAACAAGGAGGAAGCTCGAGTA | 600 | PR | 05-MAR-1999; 99US-0123180P. | |
| QY | 656 TATGACTGTGAGGAGGTGGCGAGAGAGAAATGATGGAAATTCTCT | 715 | PR | 09-MAR-1999; 99US-0123548P. | |
| Db | 601 TATGACTGTGAGGAGGTGGCGAGAGAGAAATGATGGAAATTCTCT | 660 | PR | 23-MAR-1999; 99US-0125788P. | |
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| Db | 661 TTTTAAAGGAGGAGAACTGGAGGAGCCATGCACTGAGTTAGGCTCATGATC | 720 | PR | 29-MAR-1999; 99US-0126785P. | |
| QY | 776 GGGGAGGATTTATGTTGAGCTGATGGAGAATGACAGATGGCTTAGGTTA | 835 | PR | 01-APR-1999; 99US-0127462P. | |
| Db | 721 GGGGAGGATTTATGTTGAGCTGATGGAGAATGACAGATGGCTTAGGTTA | 780 | PR | 05-APR-1999; 99US-0128234P. | |
| QY | 836 AAACCATGCACTTAACTAGCACTGCTTCAACTAAACGATAGCTGAGAGC | 895 | PR | 08-APR-1999; 99US-0131449P. | |
| Db | 781 AAACCATGCACTTAACTAGCACTGCTTCAACTAAACGATAGCTGAGAGC | 840 | PR | 16-APR-1999; 99US-0132048P. | |
| QY | 895 AATGGTCACTGCACTTGTGACAGAGAGAAACCAAAGCACTGTCAG | 955 | PR | 19-APR-1999; 99US-0132407P. | |
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| FT | | /tag= n /number= 7 |
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| FT | intron | |
| FT | | /tag= m /number= 6 3655 . 3987 |
| FT | exon | /tag= n /number= 7 |
| XX | DE19907598-A1. | |
| XX | PR | 22-FEB-1999; 99DB-01007598. |
| XX | PA | 24-AUG-2000. |
| XX | DR | WPI; 2000-566218/3. P-PSSB; AAB10674. |
| XX | PS | Claim 1; Page 10-13; 14pp; German. |
| CC | CC | This invention describes a novel DNA sequence (I) containing the coding region for an FKBP (FK506-binding protein)-like twisted dwarf protein (II) of <i>Arabidopsis thaliana</i> which has plant growth regulating activity. |
| CC | CC | (I) (or their fragments and derivatives) are used for transforming prokaryotic or eukaryotic cells, homologous recombination or for expression of a non-translated RNA that, by antisense, co-suppression or ribozyme activity, inhibits one or more endogenous FKBP-like genes in a cell, altering the responsiveness of plants (or their precursors or derivatives) and their signal transduction and reception, for altering ethylene-induced gravitropic reactions in roots or ethylene-mediated signal transduction of the graviprotic stimulus and for altering the extension growth and growth orientation of plants to change plant architecture. Also (I) can be used to identify related sequences in other plants by hybridization under low stringency conditions or by polymerase chain reaction (PCR), and to generate transgenic plants that are useful for studying the activity and signal-transduction processes of immunosuppressants (e.g. FK506, cyclosporin A, rapamycin and related compounds). This sequence encodes the <i>Arabidopsis thaliana</i> FKBP twisted dwarf protein which is described in the method of the invention |
| XX | SQ | Sequence 3999 BP; 1189 A; 697 C; 845 G; 1268 T; 0 U; 0 Other; |
| QY | Query Match | 34 7%; Score 440 6; DB 3; Length 3999; Best Local Similarity 69 6%; Pred. No. 3.6e-118; Matches 822; Conservative 0; Mismatches 19; Indels 340; Gaps 3; |
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| Db | 2819 | TGTGCTAAGAGTGAATGTCGTGAGACAGAGAAAGACTAGCGGTTAGC 2878 |
| QY | 479 | CATCGTGTGTACATGAGTCGCTGGTCAAGCTGGCTGTGCTGTGCTGGATT 538 |
| Db | 2879 | CATCGTGTGTACATGAGTCGCTGGTCAAGCTGGATT 2938 |
| QY | 539 | AGCTTATGCGAAAGAGAAACTTCTTCCATGTTCCACCTATGCCAGACTTGT 598 |
| Db | 2939 | AGCTTATGCGAAAGAGAAACTTCTTCCATGTTCCACCTATGCCAGACTTGT 2998 |
| QY | 599 | ATATCGTGGAGAAGTATGGTTGTGAAACAAAG 636 |
| Db | 2999 | ATATCGTGGAGTATGGTTGTGAAACAAAGGAGTAATTCCTATACCA 3059 |
| Db | 637 | - - - - - 636 |
| QY | 3119 | ACCTCTCTGACTTAGATGATGTTGAAAGGGAAAGCTGCAGTGATACTGAG 3178 |
| Db | 668 | GGAAGGATGGTGCAGCAGACAGAGAAAATSGATGGGATCTCTTTAAGGAGA 727 |
| QY | 3239 | GAACCTGGAGGACCATGCAAGTATGAAATGGTTATGCCATCTCTATCTAC 3298 |
| Db | 728 | GAAGCTGGAGGACCATGCAAGTATGAAATGGTTATGCCATCTCTATCTAC 727 |
| QY | 3179 | GGAAAGGATGGTGCAGCAGACAGAGAAAATSGATGGGATCTCTTTAAGGAGA 3238 |
| Db | 761 | - - - - - 760 |
| QY | 3299 | TCTCTTCCACANTTACGGTCAAAGTTAGGTTTCAGGATACTTGAGCTGTC 3358 |
| Db | 761 | - - - - - 767 |
| QY | 3359 | GAGGCTCTGTGCTCTTGGCTTGTAGTCACTGTTTGCTGTTTCAGGCCA 3418 |
| Db | 768 | GCATACATGGGGAGATTATGTTCGCTGTATGGAGTACCTGAGATATGCTTA 827 |
| Db | 3419 | GCATACATGGGGAGATTATGTTCACTGTTAGGGAGTATGGCTTA 3478 |
| QY | 828 | GCAGTAAACCCATGCCATCTAACATAGCAGTGGCTCATCAAATAAGGATC 887 |
| Db | 3479 | GCAGTAAACCCATGCCATCTAACATAGCAGTGGCTCATCAAATAAGGATC 3538 |
| QY | 888 | GATGAGCAATTGGTACTGCGAACATT----- 914 |
| Db | 3539 | GATGAGCAATTGGTACTGCGAACATT----- 914 |
| QY | 915 | - - - - - GTGT 918 |
| Db | 3599 | TCTTAAGTCATACTCGTTCTCGAAATTAATCAAACCTTATCAGGTGT 3658 |
| QY | 919 | TGACAGAAGAGAAACCCAAAGACACTGTTGAGAGGGAAAGGAGAGG 978 |
| Db | 3659 | TGACAGAAGAGAAACCCAAAGACACTGTTGAGAGGGAAAGGAGAGG 3718 |
| QY | 979 | TAGGACAGTGGACTCAGGAGCTGATGTTCCAAAGGACAAGAATGCTCTGAC 1038 |
| Db | 3719 | TAGGACAGTGGACTCAGGAGCTGATGTTCCAAAGGACAAGAATGCTCTGAC 3778 |
| QY | 1039 | ACAGGGGATTAGAGAGACCTACAGGACTTGCGAGAGAGAAAGCTGTACCAA 1098 |
| Db | 3779 | ACAGGGGATTAGAGAGACCTACAGGACTTGCGAGAGAGAAAGCTGTACCAA 3838 |
| QY | 1099 | AGCAGAAGAGAAATGCAAGAGAATTCAGGAAAGATGAGGTGGCTAAGTCAA 1158 |
| Db | 3839 | AGCAGAAGAGAAATGCAAGAGAATGAGGTGGCTAAGTCAA 3898 |
| QY | 1159 | AGACCTTTTGTGTGATGAGTGTATGCCATGTTGTTCTCTTCTCCGTATCT 1218 |
| Db | 3899 | AGACCTTTTGTGTGATGAGTGTATGCCATGTTGTTCTCTTCTCCGTATCT 3958 |
| QY | 1219 | TTCAGGCCAGAGACTAAGAGAAATGAGAG 1259 |
| Db | 3959 | TTCAGGCCAGAGACTAAGAGAAATGAGAG 3999 |
| RESULT 4 | ABX88982 | |
| ID | ABX88982 | standard; cDNA; 281 BP. |
| XX | ABX88982; | |

XX XX
 XX DT 24-APR-2003 (first entry)
 XX DB Corn ear-derived polynucleotide (cpd) #7442.
 XX KW Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;
 structural gene; functional gene; regulatory gene;
 corn ear-specific profile; gene transcription; gene expression;
 hybrid plant; desirable trait expression; plant breeding program;
 inheritance; desired characteristic; growth; development;
 disease resistance; environmental adaptability; quality; yield;
 multigene trait; plant; gene; ss.
 XX OS zea mays.
 XX PN US6476212-B1.
 XX PD 05-NOV-2002.
 XX PF 14-MAY-1999; 99US-00313294.
 XX PR 26-MAY-1998; 98US-0086722P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 XX PI Laligudi RV, Ito LY, Sherman BK;
 XX DR WPI; 2003-208840/20.
 XX PT Novel purified corn-ear derived polynucleotide useful as hybridization
 probe for detecting polynucleotide in sample, and for identifying,
 evaluating, and altering desired characteristics associated with growth,
 development.
 XX PS Example; SEQ ID NO 7442; 390pp; English.

The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (*Zea mays*) cDNA libraries SATMON022 and SATMON023. Some of the cdps uniquely identify structural, functional, and regulatory genes of corn ear. The Polynucleotides sequences are useful for detecting cdps in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breeding programs. Preferably, the cdps are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality, and yield of corn. The cdps are also useful as molecular markers for studying inheritance and multigene traits in a plant breeding program. The cdps are useful for producing purified corn-ear polypeptides by recombinant techniques. They are also useful in diagnostic assays to detect or confirm conditions or diseases associated with abnormal levels of cdps expression. ABX81541-ABX81140 represent corn ear-derived polynucleotides (cdps) of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPRO web site at seqdata.uspto.gov/pst/pipditory.html

XX Sequence 281 BP; 95 A; 44 C; 73 G; 68 T; 0 U; 1 Other;
 Query Match 12.1%; Score 154; DB 7; Length 281;
 Best Local Similarity 76.4%; Pred. No. 1.28-34;
 Matches 201; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 642 AAGCTCGCGGTGATGACTGAGGAGGATGGTCAGAGAGGAATG 701
 2 AAATCCGAGTGCATGACAGTGAGGAGGATTCAGCTGAGAGAAGATT 61

Db 62 GAGGGCAATGCATATTCAAGAAAGAGCTGAGGGGCCATGCACCATATGAAATG 121
 QY : 762 GCATAGATACTATGGGGACATTATGTTTCAAGTGAGTACAGGATAG 821
 Db 122 GCGATTGCATACATGGAGATGATTCATGTTCAATGTTGAAGTAGAGACATG 181
 QY 822 GCTTAGCAGTAAACCCATGCCCTAACATAGCAGCTGCCCATCAAACAAA 881
 Db 182 GCTTGCTGTAATCCATGCTGATGCCATGTC-AANTAAAG 240
 QY 882 CGATACGTAAGCAAGCTATGGTCA 904
 Db 241 AGATCGAAGAAGCTATGGCA 263

RESULT 5
 ABN98523 ID ABN98523 standard; DNA; 968 BP.
 XX AC ABN98523;
 XX DT 01-AUG-2002 (first entry)
 XX DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 291.
 XX Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
 KW disease; crop; thale cress; tolerance factor; insect; pathogen;
 KW nutrition; db.
 XX OS Arabidopsis thaliana.
 XX PN US2002023281-A1.
 XX PD 21-FEB-2002.
 XX PP 26-JAN-2001; 2001US-0077045.
 XX PR 27-JAN-2000; 2000US-0178472P.
 XX PA (GORL//) GORLACH J.
 PA (ANYY//) AN Y.
 PA (HAMI//) HAMILTON C M.
 PA (PRIC//) PRICE J L.
 PA (RAIN//) RAINES T M.
 PA (YUYU//) YU Y.
 PA (RAME//) RAMERKA J G.
 PA (PAGE//) PAGE A.
 PA (MATH//) MATHEW A V.
 PA (LEDF//) LEDFORD B L.
 PA (WOES//) WOESSNER J P.
 PA (HAAS//) HAAS W D.
 PA (GARC//) GARCIA C A.
 PA (KRIC//) KRICKER M.
 PA (SLAT//) SLATER T.
 PA (DAVI//) DAVIS K R.
 PA (ALIE//) ALLEN K.
 PA (HOFF//) HOFFMAN N.
 PA (HURB//) HURBAN P.

XX PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y, Haas WD;
 PI Rameka JG, Page A, Mattheu AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX DR WPI; 2002-403163/43.

PT New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of protein.
 PT
 XX
 PS Claim 1; SEQ ID NO 291; 49pp + Sequence Listing; English.
 CC The invention relates to an Arabidopsis thaliana nucleic acid (I)

WO200157207-A2.
09-AUG-2001.
05-FEB-2001; 20001WO-US003733.
04-FEB-2000; 2000US-0180403P.
28-MAR-2000; 2000US-0192745P.
(CORI-) CORIXA CORP.
Algate PA, Mannion J;
WPI; 2001-488879/53.
New polynucleotides encoding ovarian tumor proteins, useful for treating ovarian cancer, and as probes, primers, and markers of cancer

Sequencing 900 bp; 260 A; 105 C; 214 G; 303 T; 0 U; 0 C; 114 I;

Query Match 10.0%; Score 126.6; DB 6; Length 968;
 Best Local Similarity 77.7%; Pred. No. 2.4e-26;
 Matches 178; Conservative 0; Mismatches 49; Indels 2; Gaps 2;

| | | |
|----|--|-----|
| Qy | AATGGCTCTTGGAAAGAGAAAAGAACTAGCCGTTTGGCATCGGGTGTGTA | 436 |
| Dp | | 68 |
| Qy | AATGGCTCTTGGAAAGAGAAAAGAACTAGCCGTTTGGCATCGGGTGTGTA | 68 |
| Qy | TGAAGTCCTGGAAACGCCGCTTGCGATGTCGGAA-TAACCTATGGAAAGAA | 495 |
| Qy | | 496 |
| Db | TCACTCTGGTGAACGCTGCCTCTGCGATGTCGGAAATTAGCTATGGAAAGAA | 127 |
| Db | | 128 |
| Qy | TCACTCTGGTGAACGCTGCCTCTGCGATGTCGGAAATTAGCTATGGAAAGAA | 187 |
| Qy | GGAACATTTCT-TTTCCAAATGTCACCTATGGCGACTGTGATATAGGGTGGAGT | 555 |
| Db | | 555 |
| Db | GGAACATTTCT-TTTCCAAATGTCACCTATGGCGACTGTGATATAGGGTGGAGT | 613 |
| Qy | GGAACATTTCT-TTTCCAAATGTCACCTATGGCGACTGTGATATAGGGTGGAGT | 613 |
| Db | | 188 |
| Qy | TATGGCTTGATGAAACAAGAGGAGAAAGCTCGAGTGTATGACGCTGAAGT | 247 |
| Qy | | 614 |
| Db | TATGGCTTGATGAAACAAGAGGAGAAAGCTCGAGTGTATGACGCTGAAGT | 662 |
| Db | | 248 |
| Qy | TGTGGATTGATGAAAGAGGAGGAGCTTGTGATGATATT | 296 |

RESULT 6
AA625522 ID AA625522 standard; cDNA; 623 BP.

xx
AC
xx
DT
xx
xx
NAS25522;
07-NOV-2001 (first entry)

XX Human ovarian PCR-subtracted cDNA library clone #1607.
KW Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
KW gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
KW dimer; probe.

| | | |
|--|---|---|
| SQ | Sequence 1380 BP; 388 A; 318 C; 414 G; 260 T; 0 U; 0 Other; | XX |
| | Query Match 4.5%; Score 56.8; DB 7; Length 1380; | PR 12-MAR-1999; 99US-0124270P. |
| Best Local Similarity 47.5%; Pred. No. 8.7e-06; | XX | PA (HUMA-) HUMAN GENOME SCI INC. |
| Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3; | XX | PI Rosen CA, Ruben SM; |
| Db | 471 GGTTAGCCCTCGGTGTTGCTAGTGAACCTGGTGAACGCTTGCGATGTGCC 530 | XX |
| Qy | 607 GGTCTGGAGGGCATTGCGCATGGAGAAAGAGAACATTCATCGTGTACCTCAAG 666 | DR DR-P-PSDB; AAB58737. |
| Db | 531 TGGGATTACTTATGGAAAGAAAGAACCTTCTTCCAAAGTTCACCTATGCA 590 | XX |
| Qy | 667 CCCAGCTATGCTTGGAGCTGGTGGAGAAAGGT--CCAATCCACCAATCT 723 | PT PT |
| Db | 591 GACTGTGTTATGAGCTGGTGAAGTATGGCTTGTGAACAAACAGAGCTGCG 650 | PT PT |
| Qy | 724 GAGCTGAATAATGAAATTACACCTCAAGAGTTGAAAGGCCAAGGG----TCT 774 | PS PS |
| Db | 651 AGTGTATGACTGAGGAAAGATGGCAGCAGAGAGAAAATGGTGGAT 710 | XX |
| Qy | 775 TGAGGATGATTGAGAGAAAGCTGGACACCTAGTGAAGAGCGGGACT 834 | CC CC |
| Db | 711 TCTCTTTAGGAGGAGAACTGGAGGAGCCATGCAAGAGTGAATGGCCTATGCA 770 | CC CC |
| Qy | 835 GTGTACTTCAGGAGGAAATACAGCAGCTTACTACAGTAAAGAGATGCT 894 | CC CC |
| Db | 771 TACATGGGACGAGTTAGTGTTCAGCTGTTATGGCTGAGGATGGCTTASCA 830 | CC CC |
| Qy | 895 TGGCTGAATATGACTGCTAGTT-----TCAATGAGGAGCACAGAGCACGCC 948 | CC CC |
| Db | 831 GTTAAAAACCCATGCCATTAACATAGGAGCTGCTCATCAAACTAAACATACAT 890 | CC CC |
| Qy | 949 CTTCGACTGGCCTCTCACCTCACCTGGCTGTCTGAACTAGCAGGCTCT 1008 | CC CC |
| Db | 891 GAAGCAATGCTACTGCACATGTGTACAGAGAGAAAACCCAAAGACTG 950 | CC CC |
| Db | 1009 GCTGCCATTCAGAACGGCTGTAACTGGACACAACAGAGAAGGGCTC 1068 | CC CC |
| Qy | 951 TTCAAGAGAGGAAAGCAAAAGGAGCAGAGCTGGACACTGGCTGAGTGTTC 1010 | CC CC |
| Db | 1069 TTCCCCGGGAGAGCCCCTCTGCCCCATGACTTCAACTGCAGGGCTGATTIC 1128 | CC CC |
| Qy | 1011 CGAAGGCAAAAGTATGCTCTGAGGAGGAGGATGAGAGACT 1060 | CC CC |
| Db | 1129 CAGAAGGTCCTGCACTCACCCACAAACAAAGCCAGGCCAGCT 1178 | CC CC |
| RESULT 9 | | XX |
| AAP21640 | | Sequence 1903 BP; 478 A; 470 C; 528 G; 427 T; 0 U; 0 Other; |
| ID AAP21640 standard; DNA; 1903 BP. | Query Match 4.5%; Score 56.8; DB 3; Length 1903; | PR 12-MAR-1999; 99US-0124270P. |
| XX | Best Local Similarity 47.5%; Pred. No. 1e-05; Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3; | PA (HUMA-) HUMAN GENOME SCI INC. |
| AC | 531 TGGGATTACTTATGGAAAGAGGAACCTTCTTCCAAAGTGTCCACCTATGCA 590 | PI |
| XX | Db 506 CCCAGCTATGCTTGGAGCTGGAGAAACT--CCAATCCACCAATGT 562 | Rosen CA, Ruben SM; |
| DT 27-MAR-2001 (first entry) | Qy 591 GACTGTGTTATGAGGAGCTTGGAGTATTGGTTGATGAAACAAAGGGAAAGCTCGC 530 | XX |
| XX | Db 563 GAGGTGAATAATGATGATCACCTCAAGAGTTGAAAGGCCAGGIG----TCT 613 | PR 12-MAR-1999; 99US-0124270P. |
| DE Human breast and ovarian cancer associated antigen gene SEQ ID 27. | Qy 651 AGTGTATGACTGAGGAAAGATGGTGGAGCAGAGAGAAAATGGATGGAAAT 710 | PA (HUMA-) HUMAN GENOME SCI INC. |
| XX | Db 614 TGAGGATGAACTCAGAGAGAGCTGCAACAGAGCACCATGAAAGAGCGGGACT 673 | PI |
| KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; anti-allergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiotonic activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and antagonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and infectious diseases. | XX | |
| XX | Db 674 GTGTACTTCAGGAGGAAATACACAGCAAGCTTACAGTATGAAATGGCT 733 | PT PT |
| KW Addison's disease; allergy; auto-immune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease; ds. Homo sapiens. | Qy 771 TACATGGGAGGACATTATGTTCACTGTAGGGAGTAGCAGGATATGGCTTGA 830 | PT PT |
| XX | Db 734 TGGTGGATGATGAGTTGTT-----TCAATGAGGAGCACGAAAGCACGCC 787 | PS PS |
| OS | Qy 831 GTTAAACCCATGCCCTCTACATGAGCTGCGTCATCAAACAGATGAT 890 | XX |
| PN WO20055173-A1. | Db 788 CTTCGACCTGGCCTCTCACCTCACCTGGCATGTGCTATGAAACTACAGGCCCTCT 847 | XX |
| XX PD 21-SEP-2000. | Qy 891 GAAGCAATGGTCACTGCAACATGTGTGAGAGAGAAACCAAGACCTG 950 | XX |
| PP 08-MAR-2000; 2000WO-US005881. | | |

| | |
|----|---|
| CC | inflammation chronic in a tissue; M4 is useful for detecting an inflammation especially chronic in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences |
| CC | RESULT 10 |
| CC | ABK84110 standard; cDNA; 2156 BP. |
| CC | ID ABK84110; |
| CC | AC XX |
| CC | DE XX |
| CC | DT 14-AUG-2002 (first entry) |
| CC | XX |
| CC | DE Human cDNA differentially expressed in granulocytic cells #681. |
| CC | XX |
| CC | KW Human; ss: granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy. |
| CC | XX |
| CC | OS Homo sapiens. |
| CC | XX |
| CC | PN WO200228999-A2. |
| CC | XX |
| CC | PD 11-APR-2002. |
| CC | XX |
| CC | PR 03-OCT-2001; 2001WO-US0310821. |
| CC | XX |
| CC | (GENE-) GENE LOGIC INC. |
| CC | XX |
| CC | PI Baizer-Barclay Y, Weissman SM, Yamaga S, Vockley J; |
| CC | DR WPI; 2002-435328/46. |
| CC | XX |
| CC | PT Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity. |
| CC | XX |
| CC | PS Claim 1; SEQ ID NO 681; 114pp; English. |
| CC | XX |
| CC | The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an |
| CC | XX |
| CC | CC RESULT 11 |
| CC | ACCS0146 |
| CC | ID ACCS0146 standard; cDNA; 2156 BP. |
| CC | XX |
| CC | AC ACCS0146; |
| CC | XX |
| CC | DT 12-JUN-2003 (first entry) |
| CC | XX |
| CC | DE Breast cancer associated cDNA sequence SEQ ID NO:139. |
| CC | XX |
| CC | KW Human; breast cancer; cytostatic; gene therapy; gene; ss. |
| Db | 951 TTGAGAAGGGAAAGCAGAACAGAGCTAGGAGACTCGCAGCTGTATTC 1010 |
| Db | 908 TTCCGCCGGGAGAGGCCACCTGGCGTAGACTTGAGCTTGAATGCTTC 967 |
| Db | 1011 CGAAGGCAAAAGTATGCTCTGAGCAAGGGATGAGAGCT 1060 |
| Db | 968 CAGAGGGCTGCACTTACCCCAACACAAGCGGCCAGCCAGCT 1017 |

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Run on: July 7, 2004, 15:39:14 ; Search time 8003 Seconds
 Perfect score: 1270
 Sequence: 1 gaaagtccgggtcttt.....atgaaaagggttacaattt 1270
Scoring table: IDENTITY_NUC
 Gapop 10_0 , Gapext 1.0
Searched: 3470272 seqs, 2167151695 residues
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

| Database | GenBank: |
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| | * |
| 1: | gb_ba:* |
| 2: | gb_htg:* |
| 3: | gb_in:* |
| 4: | gb_om:* |
| 5: | gb_ov:* |
| 6: | gb_pat:* |
| 7: | gb_ph:* |
| 8: | gb_pl:* |
| 9: | gb_pr:* |
| 10: | gb_ro:* |
| 11: | gb_sb:* |
| 12: | gb_BY:* |
| 13: | gb_ph:* |
| 14: | gb_vl:* |
| 15: | em_ba:* |
| 16: | em_fun:* |
| 17: | em_hum:* |
| 18: | em_in:* |
| 19: | em_mui:* |
| 20: | em_om:* |
| 21: | em_or:* |
| 22: | em_ov:* |
| 23: | em_pat:* |
| 24: | em_ph:* |
| 25: | em_pl:* |
| 26: | em_ro:* |
| 27: | em_sbs:* |
| 28: | em_uni:* |
| 29: | em_vir:* |
| 30: | em_hig_hum:* |
| 31: | em_htg_inv:* |
| 32: | em_hig_other:* |
| 33: | em_hig_mus:* |
| 34: | em_htg_pnt:* |
| 35: | em_hig_rnd:* |
| 36: | em_hig_mam:* |
| 37: | em_htg_vrt:* |
| 38: | em_BY:* |
| 39: | em_higo_hum:* |
| 40: | em_higo_mus:* |
| 41: | em_higo_other:* |

Pred. No. is the number of results predicted by chance to have a

| | |
|---|--------------------------------------|
| RESULT | 1 |
| LOCUS | AX034542 |
| DEFINITION | Sequence 2 from Patent DE19907598. |
| ACCESSION | AX034542 |
| VERSION | AX034542.1 |
| KEYWORDS | GI:10303140 |
| SOURCE | Arabidopsis thaliana (thale cress) |
| ORGANISM | Arabidopsis thaliana |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis | |
| REFERENCE | 1 |
| AUTHORS | |
| JOURNAL | Patent: DE 19907598-A 2 24-AUG-2000; |

| | | | |
|-----------------------|--|--|--|
| ORIGIN | polyA_signal | KSKSLFWLIVLWQWFVSLPSR1FRRHRVKAD" | |
| | 1346..1360 | /gene="FKBP-like" | |
| Query Match | 99.6%; Score 1252.2; DB 8; Length 1360; | | |
| Best Local Similarity | 99.7%; Pred. No. 0; Mismatches | | |
| Matches | 1265; Conservative 0; Indels 3; Gaps 1; | | |
| QY | 2 AAGACTGAGGGTCTTATATTTCAGGATCAAACTGAAATTATCTCGGTG 61 | QY | 1021 AARAGTAGTCCTCCGAGACAAGGGCATAGAGAGAGAGCTACAGCAGTCAGTGATGTTCCGAAAGGCAC 1020 |
| Db | 1 AAAGTGGAGGTCTTATATTTCAGGATCAAACTGAAATTATCTCGGTG 60 | QY | 1021 AAAGTATOCCTCCGAGACAAGGGCATAGAGAGAGAGCTACAGCAGTCAGTGATGTTCCGAAAGGCAC 1080 |
| QY | 62 ATCCAGTCTCTGTGAGTCTGAGACAGCAGGAGTCACACTACTCTGACTTC 121 | QY | 1081 AGAAAGCTGTACCAAGAGCAAAATGACAGAGATAAGGAAATTAAAGGAAAGATGACAGAACATGAAATTTCCTCGGTG 1140 |
| Db | 61 ATCCAGTCTCTGTGAGTCTGAGACAGCAGGAGTCACACTACTCTGACTTC 120 | QY | 1081 AGAAAGCTGTACCAAGAGCAAAATGACAGAGATAAGGAAAGATGACAGAACATGAAATTTCCTCGGTG 1140 |
| QY | 122 ATACTTCACCCAGGTGATTGGAAATAATGGTGAATCTGAGCATCAA 181 | QY | 1141 AAGGTGTCGTAAGTCAGGAGCTTTCGAGGCACAGACGTTAAAGCAGATAAGCAGATAATGATGAGAG 1200 |
| Db | 121 ATACTTCACCCAGGTGATTGGAAATAATGGTGAATCTGAGCATCAA 180 | Db | 1141 AAGGTGTCGTAAGTCAGGAGCTTTCGAGGCACAGACGTTAAAGCAGATAATGATGAGAG 1200 |
| QY | 182 CACATGACCAAGAGAGCAAAACTCGACACAAATTGAGGATACATGGCAT 240 | QY | 1201 CCCTTTCTCCCGTATCTTGAGGCACAGACGTTAAAGCAGATAATGATGAGAG 1260 |
| Db | 181 CACATGACCAAGAGAGCAAAACTCGACACAAATTGAGGATACATGGCAT 240 | QY | 1201 CCCTTTCTCCCGTATCTTGAGGCACAGACGTTAAAGCAGATAATGATGAGAG 1260 |
| QY | 241 CTCAGAGGCTTAATGTTCTCTAAAGTGTAGTGAAAGCTGAGAAG 300 | QY | 1261 GTTACAATT 1269 |
| Db | 241 CTCAAGAGGGTAAATGTTCTCTAAAGTGTAGTGAAAGCTGAGAAG 300 | Db | 1261 GTTACAATT 1269 |
| QY | 301 TCACTAAGCGATTAAAGAGAAAGTCACGGTCCAAACCTCAAGTCTACATGT 360 | RESULT 3 | |
| Db | 301 TCACTAAGCGATTAAAGAGAAAGTCACGGTCCAAACCTCAAGTCTACATGT 360 | LOCUS | AY093009 |
| QY | 361 TTGTCACTCAGGGCATGCCAAAACTCGACACAAATTGAGGATACATGGCAT 420 | DEFINITION | Arabidopsis thaliana FKBP-type peptidy-prolyl cis-trans |
| Db | 361 TTGTCACTCAGGGCATGCCAAAACTCGACACAAATTGAGGATACATGGCAT 420 | VERSION | AY093009.1 |
| QY | 421 AGCAGCAACCTATGATGTTGTTCTGAAAGAGAAAAGAAACTAGCGGTAGCA 480 | KEYWORDS | PLN 21-APR-2002 |
| Db | 421 AGCAGCAACCTATGATGTTGTTCTGAAAGAGAAAAGAAACTAGCGGTAGCA 480 | REFERENCE | AY093009 |
| QY | 481 TCGGGTTCTCTAGCATGAACTCTGCTGTAAGCTCGGCTTGGCTGCAATTAG 540 | AUTHORS | Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowler,L., Jones,T., Bahn,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Natsume,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Becker,J., Theologis,A. and Davis,R.W. |
| Db | 481 TCGGGTTCTCTAGCATGAACTCTGCTGTAAGCTCGGCTTGGCTGCAATTAG 540 | SOURCE | Arabidopsis thaliana (thale cress) |
| QY | 541 CTATGGAAAGAGAAACGTTCTTCAATGTCACCTATGGGAGACGTGTAT 600 | ORGANISM | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis; (bases 1 to 1250) |
| Db | 541 CTATGGAAAGAGAAACGTTCTTCAATGTCACCTATGGGAGACGTGTAT 600 | TITLE | Submitted (27-MAR-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA |
| QY | 601 ATGAGGTGGAGTTGGCTTGTGAAACAAAGGGGAAAGCTCGGTATATCA 660 | COMMENT | e-mail for correspondence: arab@sequence.stanford.edu |
| Db | 601 ATGAGGTGGAGTTGGCTTGTGAAACAAAGGGGAAAGCTCGGTATATCA 660 | RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of R AFL cDNAs (R AFL cDNA : "RIKEN Arabidopsis Full-Length cDNA") : Seki,M., Natsume,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K. | |
| QY | 661 CTGTAAGAGGAAAGATTTGCTGCAAGCAAGCAAGAAATTGGATGGGATTCTT 720 | | The Salk, Stanford, PEGC (SSP) Consortium members carried out the sequencing and annotation of the R AFL cDNAs: Southwick,A., Nguyen,M., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Bahn,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Becker,J., Theologis,A. and Davis,R.W. Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs. |
| Db | 661 CTGTAAGAGGAAAGATTTGCTGCAAGCAAGCAAGAAATTGGATGGGATTCTT 720 | FEATURES | Location/Qualifiers |
| QY | 721 AGGAGGAAACTGGGGCATGCCAAATTGAGGATACATGGCATAGCTGGGG 780 | Source | 1..1250 |
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ORIGIN

| | | | |
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| Query | Match Similarity | 96.2%; Score 1221.4; DB 8; | Length 1250; |
| Best Local Similarity | 99.4%; Pred. No. | 6.4e-313; | |
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| QY | 88 | GACCAAGCAGAGTCACACTACTCTGAGCTTCTCATACTTACCCAGGTTGATTGGAA | 147 |
| Db | 61 | GACCAAGCAGAGTCACACTACTCTGAGCTTCTCATACTTACCCAGGTTGATTGGAA | 120 |
| QY | 148 | ATAATGGATAATCTCTGGCATCACACTCACACATGACCAGAGAGGGAATAGT | 207 |
| Db | 121 | ATAATGGATGAACTCTCTGCAAGCATCACACATGACCAGAGAGGGAATAGT | 180 |
| QY | 208 | ACTGAGAGAGGTGCCTGTGCATAGTG-GCCATCTCAAGAGGTAATGTCCTCTAA | 266 |
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| QY | 687 | GACAGAAGAAATGATGCGAATCTCTTTAGGGAGAACTGGGAGGCCATG | 746 |
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| QY | 747 | CAACAGATGAAATGCCATAGCATACATGGGGACGTTATGTTCAAGTGTATGG | 806 |
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| QY | 807 | AACTACAGGATATGCCATTAGAGTAAACCCATGCCATCTAACATAGCAGCTGC | 866 |
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| QY | 867 | CTCATCAACTAAACCATACGATGAGCAATGTTCTGAGCTGACTGAGAA | 926 |
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| QY | 1047 | ATTAAGAGAGAGCTTACCAAGCACTGTCAGCAGAGAAGCCCTGTTGACGAA | 1106 |
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| QY | 1167 | TTTGGTGATAGTGTATGGCATATGTTGTTCCCTTCTCCCTATCTTCGAGCG | 1226 |
| Db | 1141 | TTTGGTGATAGTGTATGGCATATGTTGTTCCCTTCTCCCTATCTTCGAGCG | 1200 |
| QY | 1227 | CACGAGTTAACGAGTAATCTATGAGAAGGGTACAATT | 1269 |
| Db | 1201 | CACGAGTTAACGAGTAATCTATGAGAAGGGTACAATT | 1243 |

RESULT 4

BT001192

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

USA

</

Lee, J.M., Kim, C.J., Quach, H.L., Shim, P., Tang, C.C., Toroumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Becker, J., Theologis, A. and Davis, R.W.

Tripp, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinzaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES

source

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ORIGIN

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Matches 1114; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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1 ATGGATGAATCTCTGGAGCACTCAAACTCAAACACATGACCAAGAGCAATAGTTACT 60

QY 211 GAARGAAGTCGCCGTGTCGTAAGTG-GCCATTCAGAGGGTAAAGTGTCTCTTAAGTT 269
61 GAAGGAAGTCGCCGTGTCGTAAGTGAGCCATCTCAAGAGGGTAAAGTGTCTCTTAAGTT 120

QY 270 GATAGTGAACTGAGGTCTTGGATAGAAGGTCAAGAACGATTAAAGGGAGGTCA 329
121 GATAGTGAACTGAGGTCTTGGATAGAAGGTCA 180

QY 330 GGTTCACAACCATCAAGACTCTCATACATGCTTGTCACTACAGGGCATGGACAAAC 389
181 GTTCOCANACGATCCAGAAGTCCTCACATGCTTGTCA 240

Db 390 TCSCAGCACAAATTGAGGATACATGGCATGAGCAACCTAATGAATGGTTCTTGA 449
241 TCGAGCACAAATTGAGGATACATGGCATGAGCAACCTAATGAATGGTTCTTGA 300

QY 450 AAAGAGAAAGAAAGACTACCGGTTAGCCATCGTGTCTACATGAGTCGGAA 509
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QY 510 CGTGGCTTGTGCAATGGCTGGAAATGCTTATGAGAAAGAGAACTTCTT 569
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Db 570 CCCATGTTCCACCTATGGCAACTGTGTTATGAGGTGAGTTATGGTTGATGAA 629
421 CGGAGTGTCCACCTATGGAGACTTGTGTTATGAGGTGAGTTATGGTTGATGAA 480

QY 630 ACAAGGAGGAAAGACTCGCAGTGATACACTGTAGAGGAAGGGATGTCGAGCAGAC 689

RESULT 5

AX034545

LOCUS AX034545 Sequence 5 from Patent De19907598.

DEFINITION 1142 bp DNA linear PAT 22-SEP-2000

ACCESSION AX034545

VERSION AX034545.1 GI:10303142

KEYWORDS

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum (tomato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1

REFERENCE Patent: DE 19907598-A 5 24-AUG-2000;
SCHULZ BURKHARD (DE)

AUTHORS Location/Qualifiers
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JOURNAL

FEATURES

source

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ORIGIN

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Best Local Similarity 73.8%; Pred. No. 2..le-129;
Matches 686; Conservative 0; Mismatches 242; Indels 1; Gaps 1;

QY 199 GAATAGTGTACTGAGGAGACTCGCCTGTCAGTGCCTCATCTCGAGGGTAATGTT 257

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| Db | 211 | GAATCATCGCTGAGGGCCTCACTGTTGAGAACCTCCACAGGATGATGCTGG | 270 | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; |
| Qy | 258 | CCTCTTAAGTTGATGAGTGAAGCTGAGCTTGATGAGAAAGTCAGAACGATATA | 317 | Ehrhartoideae; Oryzeae; Oryza. |
| Db | 271 | CCGCCTAAAGATTGATTCAGAGTGAAGTACAGGAAAGTACACAGAAATTGT | 330 | REFERENCE AUTHORS |
| Qy | 318 | AAGGAGGTACCGGTTCCACACCTCCAACTCTACTCTACATGCTTTGTCACATCAGGGCA | 377 | The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shiniki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Xie,Q., Iii,M., Kuroasaki,T., Kodama,T., Masuda,H., Kobayashi,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Itoh,M., Hayashida,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Aralawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Saito,R., Sasaki,D., Sato,K., Shubata,K., Shinagawa,A., Shiraki,T., Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice |
| Qy | 438 | TGGCTCTTGAAAGAGAAGAAAGACTAGGCCGTTAGCCACGGGTTGCTPAGATG | 497 | Kagawa,I., Kondo,S., Kono,H., Miyazaki,A., Osako,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shubata,K., Shinagawa,A., Shiraki,T., |
| Db | 451 | CTGGTATAGAAAGAGAAGAAAGACTGGCTAGCTATGGCTTAACAGCATG | 510 | Yoshino,M., and Hayashizaki,Y. |
| Qy | 498 | AAGCTGGTAAACGGCGCTGTGCGATGTTGAGGATACATGGATGAGCACCATATGAA | 557 | Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice |
| Db | 511 | AAATCCGGGGAGCTGCTTATTCTATGTTGGCTGGAACTAGCTATGGAAAGAGGA | 570 | Science 301 (5631), 376-379 (2003) |
| Qy | 558 | AACCTTCTTCCCAATGTCACCTATGCACTATGAGCTTATAGAGTTGGAGTT | 617 | MEDLINE |
| Db | 571 | AACCTCTTCCCAATGTCACCTATGCACTATGAGCTTATAGAGTTGGAGTT | 630 | PUBLISHED |
| Qy | 618 | GGGTGTGANGAACRAAGGGGAAAGSTCGCAGTGTAGTGTAGGAGGAGGTT | 677 | 2 (bases 1 to 1396) |
| Db | 631 | GGCTCTGATGAGCAGGGAGGAAAGACGAGGTGACATGACAGTAGAGGAGAATT | 690 | AUTHORS |
| Qy | 678 | GCTGCAGCAGCAGAGAAAATGGTGGAACTCTCTTTAGGGAGAAACTGGAG | 737 | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanasaki,T., Hara,A., Hashidume,W., Hayashida,W., Hayatsu,N., Imotani,K., Itoh,M., Kawamura,M., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Aralawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Saito,R., Sasaki,D., Sato,K., Shubata,K., Shinagawa,A., Shiraki,T., Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice |
| Db | 691 | GGGACACGAGCATAGAGAAGATGATGATGAAATCTTTAAGGAGAAGACTGGAG | 750 | Hori,F., Hotta,I., Iida,Y., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Isono,I., Ishikawa,M., Itoh,M., Kawamura,M., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Aralawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Saito,R., Sasaki,D., Sato,K., Shubata,K., Shinagawa,A., Shiraki,T., Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice |
| Qy | 738 | GAAGGCATGAACTATGAAATGCCATAGCATACATGGGAGGATTATGTTAG | 797 | Kawamura,M., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Aralawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Saito,R., Sasaki,D., Sato,K., Shubata,K., Shinagawa,A., Shiraki,T., Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice |
| Db | 751 | GAAGGTATGCACTATGAAATGCCATGCAATGGAGATGACITCAGTTTCAG | 810 | Science 301 (5631), 376-379 (2003) |
| Qy | 798 | CTGTTGGAGTACCGGTTATGCTTAAACCCATGCCATCTAACATA | 857 | MEDLINE |
| Db | 811 | CTGTCGGTAGTCGGGACATGCCATGCTGAACTGCTGCACTGACATG | 970 | PUBLISHED |
| Qy | 858 | GCAGCTTGCTCATCAAATCTAACCGATGGATGAGCAATTGTACTGCACTTGT | 917 | 2275273 |
| Db | 871 | GCAGCTTGCTGTCGAGCTCAGCGATATGATGAGCCATTGCGCATCTGAC | 930 | (bases 1 to 1396) |
| Qy | 918 | TTGACAGAGAGAGAACCCAAAGGCTGTGAGGAGGAAGCAAGGAGCAG | 977 | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanasaki,T., Hara,A., Hashidume,W., Hayashida,W., Hayatsu,N., Imotani,K., Itoh,M., Kawamura,M., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Aralawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Saito,R., Sasaki,D., Sato,K., Shubata,K., Shinagawa,A., Shiraki,T., Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice |
| Db | 931 | CTAGCAGAGAGAACCATGTTAAAGGTTGTGAGCGTGAAGGCTTAGCTATA | 990 | REFERENCE |
| Qy | 978 | CTAGACAGATGGACTCAGGACGTCATGATGTTCCGAAAGGCAAAAGTGTGCTGAC | 1037 | AUTHORS |
| Db | 991 | CTGGCTCAGCTGATGCGAGCTCAGCGATATGATGAGCCATTGCGCATCTGAC | 1050 | The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team; Kikuchi,S., Satoh,K., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Saito,R., Sasaki,D., Sato,K., Shubata,K., Shinagawa,A., Shiraki,T., Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice |
| Qy | 1038 | GACAGGGGTTAGAGAGCTAGGACTCTCTTAAGCACCTAAGTGTGCTACCA | 1097 | COMMENT |
| Db | 1051 | GATAAGCCATACAGGGATTGATTGATGCGAGAACACGAGAGGCTGTCTTACAA | 1110 | This clone is one of the 28K full-length cDNA clones from Japonica rice. URL : http://cdna01.dna.afrc.go.jp/cDNA/ |
| Qy | 1098 | AAGCAGAAAGAAATGACAAGGATT | 1126 | NIAS Rice Full-Length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yohagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., and Yamanoto,M. |
| Db | 1111 | AAACAAAGGAACTTACAAGGATT | 1139 | FAIS Genome Sequencing & Analysis Group; Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamura,M., Kobayashi,M., Kodama,T., Kurokawa,T., Kusunegi,T., Itoh,M., Mizuno,K., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matubara,K., and Murakami,K. |
| RESULT | 6 | AK065114 | AK065114 | DEFINITION Oryza sativa (japonica cultivar-group) mRNA clone:J013001006, full insert sequence. |
| ACCESSION | | AK065114 | AK065114.1 | VERSION AR065114.1 GI:32975132 |
| KEYWORDS | | FIL_CDNA; CAP_trapper; | Oryza sativa (japonica cultivar-group) | |
| SOURCE | | | Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., | |
| ORGANISM | | | | |

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 Best Local Similarity 69.9%; Pred. No. 1.2e-108;
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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| QY | 761 | ----- | 760 | |
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| Db | 3599 | TCATAAAGTCATACTCGTTCTGAAATCTAATCAAACTAAACCTTACGGGT | 3658 | |
| QY | 919 | TGACAGAAGAGGAAACCCAAAGACTGTTGTCAGAGGAGGAACGCAAGCAGC | 978 | |
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| QY | 1099 | AGCGAGAAGAAATCTACAGAGGAAATTCAAGCGAGAGCTGCAAGAGAGCTTACCAA | 1158 | |
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| QY | 479 | CATCGGTGTTGCTAGCATGAGTCGGAGACCTGGCGMTGCGATGTTGCTGCGCTTGCGTGGAAATT | 538 | Db | 56753 | | TTGCACGCCACAGAGTTAACAGGATTAAGCAGATAATGTTAAGGAAGGCTAACATT | 56703 |
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| Db | 57593 | ACCTCTGACTTAGATGATGTTGAGCTTATGAAAGCTTATCCACCTCTTGCTT | 57534 | | | | | |
| QY | 668 | GGAAGGATTGGTGCAGCACAGAACAGAAATGGATGGAACTCTTTAGGAGA | 727 | | | | | |
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| Db | 56933 | ACAAGGGATTTGAGAGAGCTACAGACCTTGCAGAGAGAGAAAGCTTGACAA | 56874 | | | | | |
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| QY | 1159 | AGACCTTTTGGTGTAGTGTATGCAATGCTGTTCTTCTCCGTACT | 1218 | | | | | |
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| SOURCE | Unknown. | | | | | | | |
| ORGANISM | Zea mays | | | | | | | |

| REFERENCE | Unclassified. |
|------------|---|
| AUTHORS | 1. (bases 1 to 281) Laligui, R.V., Ito, L.Y. and Sherman, B.K. |
| JOURNAL | Polynucleotides and polypeptides derived from corn ear |
| FEATURES | Patent: US 6476212-A 05-NOV-2002; Location/Qualifiers 1. .281 /organism="unknown" /mol_type="genomic DNA" |
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| LOCUS | AP006144 121882 bp DNA linear PLN 2-JUL-2003 |
| DEFINITION | Lotus corniculatus var. japonicus genomic DNA, chromosome 3, |
| ACCESSION | AP006144 clone LJ1T23P21, FM0261, complete sequence. |
| VERSION | AP006144.1 GI:29122781 |
| SOURCE | HTG. |
| ORGANISM | Lotus corniculatus var. japonicus (Lotus japonicus) |
| KEYWORDS | Lotus corniculatus var. japonicus Bukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaceae; Lotus. |
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| LOCUS | AC136506 135457 bp DNA linear PLN 09-MAY-2003 |
| DEFINITION | Medicago truncatula clone mth2-33c8, complete sequence. |
| ACCESSION | AC136506 AP006144 |
| VERSION | AC136506.9 GI:30468006 |
| SOURCE | HTG. |
| ORGANISM | Medicago truncatula (barrel medic) |
| KEYWORDS | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliae; Medicago. |
| RESULT 14 | Query Match 12.1%; Score 154; DB 6; Length 281; Best Local Similarity 76.4%; Pred. No. 1e-29; Matches 201; Conservative 0; Mismatches 61; Indels 1; Gaps 1; |
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| DEFINITION | 2 AAATCCGAGTGCAGATGACAGTGGAGAGGATTGCAAGAGAAGATG 61 |
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| VERSION | 62 GAGGCGAATGCAATTCTCAAGAAAGAAGANGCTGGAGGCCATGAGCAATGAAATG 121 |
| SOURCE | Db 62 GAGGCGAATGCAATTCTCAAGAAAGAAGANGCTGGAGGCCATGAGCAATGAAATG 121 |
| ORGANISM | 762 GCCATAGCATAGGGAGCAGTTATGTTAGCTGAGCTGTATGGAAAGGACTTC |
| KEYWORDS | 182 GCCTTGCTGTGAAATCATGCCTCAATATGGCTGATGCTGATC-AANTTAAG 240 |
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| TITLE | Db 241 AGATTCGATGAGGATGCTCA 263 |
| RESULT 15 | Query Match 11.8%; Score 150.2; DB 8; Length 121882; Best Local Similarity 67.5%; Pred. No. 1; 3e-28; Matches 264; Conservative 0; Mismatches 58; Indels 69; Gaps 1; |
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| DEFINITION | 60152 TGAACAGAGAGAGAGATACTGGCTGCTGGCATGGTGGCAAGCATGAAAGCTGG 505 |
| ACCESSION | QY 60212 GAGGCGGCGCTGCGCTGGCTGGCTGGATAGGATGGAAAGAGGAAGCTTC 60271 |
| VERSION | Db 566 TTTCGCAATGTCACCATATGGCAGACTGTTAGCTATAGGGAAATAGGGAAATGTTGA 625 |
| SOURCE | Db 60272 TTTCGCAATGTCACCATATGGCAGACTGTTAGCTATAGGGAAATAGGGAAATGTTGA 60331 |
| ORGANISM | QY 626 TGAAACAAAGAAG 636 |
| KEYWORDS | Db 60332 TGAAACAAAGAAGTAAGTGTGCAATAGACTTATATGACCATGGACTTGCACAGATG 60391 |
| FEATURES | QY 637 - -----AGGAAAGCTCCAGCTATGACTGAGCTGAGGAAAGAT 676 |
| TITLE | Db 60392 CTATTGTRCTTAATTCAAGSGAAAGCTGCAGCTGATGACTGTGAGGAAAGAT 60451 |
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| AUTHORS | Db 60452 TGGTGCAAGAGCAAGTGGAGAAGATGGATGAGATGCAATGCTCTGTCAGGAAATTAACAGA 60511 |
| JOURNAL | QY 737 GGAGGCGATGCAACAGTAGATGAAATGGCCATA 767 |
| MEDLINE | Db 60512 GAAGCTATGCAACAGTAGATGAAATGGCTACA 60542 |
| RESULT 16 | Query Match 11.8%; Score 150.2; DB 8; Length 121882; Best Local Similarity 67.5%; Pred. No. 1; 3e-28; Matches 264; Conservative 0; Mismatches 58; Indels 69; Gaps 1; |
| LOCUS | AC136506/c 135457 bp DNA linear PLN 09-MAY-2003 |
| DEFINITION | AC136506 Medicago truncatula clone mth2-33c8, complete sequence. |
| ACCESSION | AC136506 AP006144 |
| VERSION | AC136506.9 GI:30468006 |
| SOURCE | HTG. |
| ORGANISM | Medicago truncatula (barrel medic) |
| KEYWORDS | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliae; Medicago. |
| RESULT 17 | Query Match 11.8%; Score 150.2; DB 8; Length 121882; Best Local Similarity 67.5%; Pred. No. 1; 3e-28; Matches 264; Conservative 0; Mismatches 58; Indels 69; Gaps 1; |
| LOCUS | AC136506 135457 bp DNA linear PLN 09-MAY-2003 |
| DEFINITION | AC136506 Medicago truncatula clone mth2-33c8, complete sequence. |
| ACCESSION | AC136506 AP006144 |
| VERSION | AC136506.9 GI:30468006 |
| SOURCE | HTG. |
| ORGANISM | Medicago truncatula (barrel medic) |
| KEYWORDS | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliae; Medicago. |
| RESULT 18 | Query Match 11.8%; Score 150.2; DB 8; Length 121882; Best Local Similarity 67.5%; Pred. No. 1; 3e-28; Matches 264; Conservative 0; Mismatches 58; Indels 69; Gaps 1; |
| LOCUS | 22570290 135457 bp DNA linear PLN 09-MAY-2003 |
| DEFINITION | 22570290 Unpublished (bases 1 to 135457) |
| ACCESSION | 22570290 Shauil,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. |
| VERSION | 22570290 Shauil,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. |
| SOURCE | 22570290 Direct Submission |
| FEATURES | 22570290 Submitted (05-NOV-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA |
| REFERENCE | 3 (bases 1 to 135457) Shauil,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. |
| AUTHORS | 3 (bases 1 to 135457) Shauil,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. |
| RESULT 19 | Query Match 11.8%; Score 150.2; DB 8; Length 121882; Best Local Similarity 67.5%; Pred. No. 1; 3e-28; Matches 264; Conservative 0; Mismatches 58; Indels 69; Gaps 1; |
| LOCUS | 12693552 135457 bp DNA linear PLN 09-MAY-2003 |
| DEFINITION | 12693552 Unpublished (bases 1 to 135457) |
| ACCESSION | 12693552 Shauil,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. |
| VERSION | 12693552 Shauil,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. |
| SOURCE | 12693552 Direct Submission |
| FEATURES | 12693552 Submitted (08-MAR-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA |
| REFERENCE | 4 (bases 1 to 135457) Shauil,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. |
| AUTHORS | 4 (bases 1 to 135457) Shauil,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A. |


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Contains HSF-type DNA binding domain signature AA69-93
contains EST gb|R65204, Aao42693"
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Contains EF-hand calcium-binding domain AA94-106, EF-hand
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contains EST gb|R65197, R87041, Aa597913"
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Matches 178; Conservative 0; Mismatches 49; Db 62887
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Qy 436 AATGGCTCTTGAAAGAGAAAAGAAACTAGCCGGTTAGCCATGGCTGTGCTGCA 62888
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Qy 496 TGAAGTCTGTTGAAACGTCGGCTCTGAGTGTGCTGGAAATTAGATAATGGAGAT 62768
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Db 62707 TGTGGATTTGATGAAACAAGGAGAAAAGTCGGAGTATGCT 62659

RESULT 15
LOCUS CNS08CDP
DEFINITION Oryza sativa chromosome 11. BAC OSJN003p03 of library OSJN03
of chromosome 11 of cultivar Nipponbare of ssp. japonica of Oryza
sativa (rice); complete sequence.
ACCESSION BX000499_AU51005
VERSION BX000499.1 GI:25900572
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryeae; Oryza.
REFERENCE I (bases 1 to 12553)
AUTHORS Choisne,N., Orjeda,G., Cattolico,L., Demange,N., Wincker,P.,
```

Segurens,B., Pelletier,E., Scarpelli,C., Salanoubat,M.,
 Weissenbach,J. and Quétier,F.
Oryza sativa chromosome 12 sequencing
 JOURNAL Unpublished
 REFERENCE 2
 AUTHORS (bases 1 to 125593)
 Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2003) Genoscope - Centre National de Séquençage : BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT On Oct 17, 2003 this sequence version replaced gi:12329146.
 Center: Genoscope / Centre National de Séquençage
 Center code: GS
 Web site: http://www.genoscope.cns.fr/
 Contact: SeqRef@genoscope.cns.fr

 The following sequence is oriented from the T7 to the sp6 end.
 ----- Finishing boundaries
 FINISHED SEGMENT STARTS AT BASE 1
 FINISHED SEGMENT ENDS AT BASE 125593

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 location/Qualifiers
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 Best Local Similarity 77.6%; Pred. No. 1.9e-21;
 Matches 149; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
 QY 450 AAAGGAAAGAACATGCCGGTTAGCCATCGGGTGCCTACATGAGTCGTGAA 509
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 QY 510 CGTGGCTGTGCGTGGCTGGAAATTAGCTTATGGAAAGAAGGAAACTTTCTTT 569
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 QY 630 ACAAGGGAGGA 641
 Db 111924 GTCAAGAGAGTA 111935

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GenCore version 5.1.6

OM nucleic - nucleic search, using SW model

Run On: July 7, 2004, 16:22:54 ; Search time 123 Seconds
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5729.981 Million cell updates/sec

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| Scoring table: | IDENTITY_NUC |
| | Gapop 10.0 , Gapext 1.0 |
| Searched: | 682709 seqs, 277475446 residues |

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Listing first 45 summaries

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SUMMARIES

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| 1 | 154 | 12.1 | 281 | 4 US-09-313-294A-7442 Sequence 7442, Ap |
| 2 | 71 | 12.6 | 7218 | 1 US-08-232-463-14 Sequence 14, Appl |
| 3 | 56.8 | 4.5 | 2157 | 1 US-08-335-618-25 Sequence 25, Appl |
| 4 | 56.8 | 4.5 | 2246 | 4 US-09-565-921-48 Sequence 48, Appl |
| 5 | 44 | 5.5 | 2291 | 4 US-09-220-132-114 Sequence 114, Appl |
| 6 | 40.6 | 3.2 | 289 | 3 US-09-007-005-17 Sequence 17, Appl |
| 7 | 40.6 | 3.2 | 289 | 3 US-09-244-796-17 Sequence 17, Appl |
| 8 | 39.8 | 3.1 | 472 | 4 US-09-621-976-973 Sequence 973, Appl |
| 9 | 37.2 | 2.9 | 5252 | 4 US-09-976-594-308 Sequence 308, Appl |
| 10 | 37.2 | 2.9 | 5712 | 4 US-09-976-594-820 Sequence 820, Appl |
| 11 | 36.8 | 2.9 | 486 | 3 US-09-338-972-90 Sequence 90, Appl |
| 12 | 36.8 | 2.9 | 486 | 4 US-09-405-065-78 Sequence 78, Appl |
| 13 | 36.8 | 2.9 | 2802 | 4 US-09-976-594-924 Sequence 924, Appl |
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| 15 | 36 | 2.8 | 3279 | 4 US-09-533-681A-2886 Sequence 2886, Appl |
| 16 | 35.8 | 2.8 | 148567 | 4 US-09-801-876B-3 Sequence 3, Appl |
| 17 | 35.8 | 2.8 | 148567 | 4 US-10-234-862-3 Sequence 3, Appl |
| 18 | 35.6 | 2.8 | 1298 | 3 US-08-948-705-3 Sequence 3, Appl |
| 19 | 35.6 | 2.8 | 1298 | 4 US-09-510-543-3 Sequence 3, Appl |
| 20 | 35.4 | 2.8 | 1664976 | 4 US-08-916-421B-1 Sequence 1, Appl |
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| 22 | 34.8 | 2.7 | 277 | 3 US-09-007-005-3 Sequence 3, Appl |
| 23 | 34.8 | 2.7 | 277 | 3 US-09-244-793-3 Sequence 3, Appl |
| 24 | 34.4 | 2.7 | 278 | 4 US-09-621-976-13872 Sequence 13872, A |
| 25 | 34.4 | 2.7 | 603 | 5 PCT-US92-01691-27 Sequence 27, Appl |
| 26 | 34.4 | 2.7 | 603 | 5 PCT-US92-01691-28 Sequence 28, Appl |
| 27 | 34.4 | 2.7 | 627 | 4 US-09-833-381-1295 Sequence 295, Appl |

ALIGNMENTS

RESULT 1
US-09-313-294A-7442
Sequence 7442, Application US/09313294A
; GENERAL INFORMATION:
; PATENT NO. 6476212
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313, 294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
SEQ ID NO 7442
LENGTH: 281
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700381733H1
NAME/KEY: unsure
LOCATION: 235
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7442

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Best Local Similarity 75.64%; Pred. No. 2, 6e-37; Mismatches 61; Indels 1; Gaps 1;
Matches 201; Conservative 0; MisMatches 61; Indels 1; Gaps 1;

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Qy 762 GGCATAGCATACATGGGGACGATTGTTCACTGGCTGATGGAAACTACAGGATATG 821
Dy 122 GCGATTGCAATCATGGGAGATATTCTGCAATTTGGAAAGTACAGAGCTG 181

Qy 822 GCTTGTAGGTAAACCCATGCCATCTAACATACAGCTGCTCATCAACTAA 881
Dy 182 GCCTTGGCTGAAATCCATGCCATCTAACATGGCTGATGCGCTGATC-AANTAAAG 240

Qy 882 CATTACGATGAGCAATGGTCA 904
Dy 241 AGATTCGATGAGCTATGCGCA 263

RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5,670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFFINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPox VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner,
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22311-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE: 26-AUG-1991
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; FILING DATE:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; IMMEDIATE SOURCE:
; CLONE: pZPgt-F1B
; US-08-232-463-14

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Db 1396 RRR 1337
QY 721 AGGAGGAGAAGACTGGAGGAGCCATGCAACAGTAGATGATCATGAGGG 780
Db 1336 RRR 1277
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Db 1216 RRR 1157

RESULT 3
US-08-336-618-25
; Sequence 25, Application US/08336618
; Patent No. 5,763590
; GENERAL INFORMATION:
; APPLICANT: Peatlie, Debra A.
; APPLICANT: Harding, Matthew W.
; APPLICANT: Livingston, David J.
; TITLE OF INVENTION: ISOLATION OF AN MR 52,000 FK506 BINDING PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN TITIIE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,618
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/963,325
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/777,752
; FILING DATE: 11-OCT-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02173
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VPP191-05A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2157 base pair B
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 100..1476
; US-08-336-618-25
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Best Local Similarity 47.5%; Pred. No. 4.6e-07; Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;
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Db 706 GGTCTGGAGGCCATTCAGGCATCGAGAAGGAGACATTCATGTCGTCACCTG 765

QY 531 TGGGATATTAGCTTGGAAAGAGAAACCTTCTTCAGTGTTCCACCTATGCCA 590
Db 766 CCCAGCTATCTTGTGGCGTGTGGGAAAGT--CCAATCCACCAATGC 822
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Db 823 GAGCTGAATATGATTACCTCAGAGTTTGTGAAAGGCCAGGG 650
QY 651 AGTGATATGACTGTAGGAGGATTTGTCAGCAGAGAAGCTGAGCCATATGAGAGGG 710
Db 874 TGGAGATGATTCAGAAGAGAAGCTGGACAGACCATAGTAAGAGGGAT 710
QY 711 TCTCTTTAAGGGAGAACCTGGAGGAACTGGAGGATGGAAATGGATGGGAT 710
Db 934 GTGACTTCAAGGAGGTTTGTGAGCTTACAGCAGCTTACTAGTAAAGATGCT 933
QY 771 TACATGGGGAGGTTTGTGAGCTTACAGCAGCTTACAGTAAAGATGCT 933
Db 994 TGGCTGAATATGAGCTTAGTTT-----TCCATGAGGAGCACAGGCC 1047
QY 831 GTTAACACCATGCAATTACATAGGCTGCTCATCAACTAAACGATACAT 993
Db 1048 CTCGACTGCCCCCTCACCTCAACTGSCCATGTCATGTAACAGGCTTCTC 1107
QY 891 GAAGCAATGTCACTGCAATGTGTCAGAGAAAACCCAAAAGACTG 950
Db 1108 GCTGCCATTGAAAGTGTGAACTGGACAGCAACACAGAAGGGCTC 1167
QY 951 TTCAAGAAGGGAAAGCAAGGGAGAGCTGAGCTGAGCACTGAGCTGATGATTIC 1010
Db 1168 TTCCGCCGGAGAGGCCACCTGCGCTGAGCTGAGCTGAGGGCTC 1227
QY 1011 CGAAGGCAAAAGTAGTGTCTGAGCAAGGGGATAGAGAGCT 1060
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RESULT 4
US-09-566-921-49
; Sequence 49, Application US/09566921

; Patent No. 6682888

; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Crila M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO: 48
; LENGTH: 2246
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; OTHER INFORMATION: Incyte ID No. 6682888 474194.5
; US-09-566-921-48

Query Match 4.5%; Score 56.8; DB 4; Length 2246;
Best Local Similarity 47.5%; Pred. No. 4.7e-07; Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

QY 471 GGTTAGGCCCTGGTGTCTAGCATGAAAGCTGGCTTGTGCTGG 530
Db 762 GGTCTGGAGGGCATTCTGGCTGAGGAAAGGAGACATTCCATCGTACAG 821
QY 531 TGGBATTAGCTTGGAAAGGAAACTTCTTCCAAATGTCACCTATGCA 590
Db 822 CCCAGCTATCTTGTGGCTGAGCTGAGGAAAGT--CCAATCCACCAATGC 878
QY 591 GACTGTGTTATGAGGTGAACTGGAGGATGGAAATGGATGGGAT 650

Db 879 GACTGTGAAATGAAATCACCTCAAGTGTGAAAGGCCAGGG-----TCT 929
QY 651 AGTGATATGACTGTAGGAAAGTGGTGTGAGCAGAGAAATGGATGGGAT 710
Db 930 TGGAGATGATTCAGAGAGCTGAGCCATATGAGAGGG 770
QY 990 GTGACTTCAAGGAGGTTTGTGAGCTTACAGTAAAGATGCT 1049
Db 771 TACATGGGGAGGTTTGTGAGCTTACAGTAAAGATGCT 830
QY 770 TGGCTGAATATGAGCTTAGTTT-----TCCATGAGGAGCACAGGCC 1103
Db 831 GTTAACACCATGCACTTACATAGGCTGCTCATCAACTAAACGATACAT 890
Db 1164 GCTGCCATTGAAAGTGTCTACAGGCCCTAGACTGAGCACTGAACTAGGCC 1223
QY 951 TTCAAGAAGGGAAAGCAAGGGAGAGCTGAGCAAGGGGATAGAGAGCT 1010
Db 1224 TTCCGCCGGAGAGGCCACCTGCGCTGAGCTGACTTGTGAGCTGAGCT 1283
QY 1011 CGAAGGCAAAAGTAGTGTCTGAGCAAGGGGATAGAGAGCT 1060
Db 1284 CAGAGGTCCTGAGCTTACCCACAAAGGCCACAGCCAGCT 1333

RESULT 5
US-09-220-132-114

; Sequence 114, Application US/09220132
; Patent No. 6506607

; GENERAL INFORMATION:

; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220-132
; CURRENT FILING DATE: 1998-12-23
; PRIORITY NUMBER: US 60/079,303
; PRIORITY NUMBER: 1998-03-25
; PRIORITY NUMBER: US 60/068,821
; PRIORITY NUMBER: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 114
; LENGTH: 2291
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-220-132-114

Query Match 3.5%; Score 44; DB 4; Length 2291;
Best Local Similarity 45.8%; Pred. No. 0.0039; Matches 281; Conservative 0; Mismatches 315; Indels 18; Gaps 3;

QY 447 GGAAAGGAGAAAAGAACTTACCGGTTAGGCCATCGGTGCTACATGAGTCGGT 506
Db 554 GGAGAGAACCCAGACATTCACATTGGAAATGCGCGCAA 613
QY 507 GAACTGGCTTGTGCACTGCTGGGAAATTAGCTTGTGGAAAGGAAACTTCT 566
Db 614 GAACTGGCTTGTGCACTGCTGGGAAATTAGCTTGTGGAAAGGAAACTTCT 673
QY 567 TTTCCTAATGTCACCTATGGCAGCTGTGATAGGGTGTGGTTGAT 626
Db 674 TTGGCA--TGAACCTATGTCAGCTTACAGTAAAGCTGCTG-- 728
QY 627 GAAACAAGGAGGAAAGCTGGCTGAGCTGATGACTGAGGAGGAGGCTCAA 686

US-09-621-976-973
; Sequence 973, Application US/09621976
; Patent No. 6633063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO: 973
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..471
; US-09-621-976-973

Query Match 3.1%; Score 39.8; DB 4; Length 472;
Best Local Similarity 50.8%; Pred. No. 0; 0,031; Mismatches 92; Indels 0; Gaps 0;
Matches 95;; Conservative 0; ; Nucleotides 95;

Qy 158 AATCTCTGCGACATCAAACTAACACATGCCAGAGGCGAATAGTTACTGAAAGCAA 217
Db 268 AAGGCCAGGTGAAGAACGCTCCGGAGAGAGCAGAATGAGTACCGGCTGAGTC 327

Qy 218 GTGCCGTGTGCATAGTGCCTCAAGGGTAATGTCTCTTAAGTGTAGTCA 277
Db 328 CTGGGCTGCGCAAGCSCCAAGGCCAGGTGTGAAATGCTGCTATTGTGATCA 387

Qy 278 AGCTGAGGCTTGATGAGAAGTCAGTAGCACATAAAGGAAGGTACGGTCCAA 337
Db 388 ATGCTCGCTTGAGGAAATCTTAAAGCAAGAGAAAGGTTACTCTAAAG 447

Qy 338 ACCATCC 344
Db 448 AAGCTCC 454

RESULT 9
US-09-976-594-308
; Sequence 308, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Furness, Jenny
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIORITY FILING NUMBER: 60/140,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program

SEQ ID NO: 308

RESULT 10
US-09-976-594-820
; Sequence 820, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIORITY FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program

SEQ ID NO: 820
LENGTH: 5712

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 427967.4
US-09-976-594-820

Query Match 2.9%; Score 37.2; DB 4; Length 5712;
Best Local Similarity 51.2%; Pred. No. 0; 0; Mismatches 83; Indels 0; Gaps 0;
Matches 87;; Conservative 0; ; Nucleotides 87;

Qy 870 ATCAACTAAAGATAGATGAGGAACTGGTCACTGCACATGGTGTGACAGAGAA 929
Db 339 ATCAGAACAAAGATCAAGACTGTTAAGCAGACTGTTAACAGCAGAG 398

Qy 930 GAGAAACCCAAAGCTGTTCAGAGAGGAAACCAAGGAGCTAGACAGATG 989
Db 399 AATATATATATATGCTGGTTTATGGCTTCGTGAGCTGACTAGAACCT 458

Qy 990 GACTCACAGCTGATGATTCGAAAGGACAAAGTATGCMCTGAGGA 1039
Db 459 GATCAGGCCAGAGTGCCTATAAAAGCTGAATTAGGCCAGCCA 508

RESULT 11
US-09-358-972-90
; Sequence 90, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppi, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: PRC-103 6868/75528
CURRENT APPLICATION NUMBER: US/09/358,972
CURRENT FILING DATE: 1999-07-22

Qy 870 ATCAAACATAAACCATACGATGAAAGCAATTGGTCACTGACATGTTGAGAGAAA 929

Query Match 2.9%; Score 37.2; DB 4; Length 5252;
Best Local Similarity 51.2%; Pred. No. 0; 0; Mismatches 83; Indels 0; Gaps 0;
Matches 87;; Conservative 0; ; Nucleotides 87;

Qy 870 ATCAAACATAAACCATACGATGAAAGCAATTGGTCACTGACATGTTGAGAGAAA 929

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; EARLIER APPLICATION NUMBER: 09/252, 436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042, 287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 90
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Pyrococcus furiosus
; US-09-358-972-90

Query Match      2.9%;  Score 36.8; DB 3; Length 486;
Best Local Similarity 56.7%; Pred. No. 0.26; Mismatches 52; Indels 0; Gaps 0;
Matches 68; Conservative 0; MisMatches 52; Del 0; Insert 0;

QY      653 TGATATGACTGTAGAGGAAGGGATGGTGCAGCAGACAGAAAATGATGGAAATC 712
Db      222 TGTTRGGGTTGAGGGAGGATGCACTGAGAAGTAGTGTAGAAGATGGCTGGACTAC 281
QY      713 TCTTTTAAGGAGGAGAAACTGGAGAACGCATCAACAGTATACTGAAATGCCATAGCAT 772
Db      282 TGATCCAAGAGCAGCACCTGGGACAAATTAGGGAGATTATGGACTTGACATAGAGA 341

RESULT 12
US-09-406-065-78
; Sequence 78, Application US/09406065
; Patent No. 6312902
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leippe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A
; APPLICANT: Hartnett, James R
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J
; APPLICANT: Welch, Roy
TITLE OF INVENTION: Improved Nucleic Acid detection
FILE REFERENCE: Improved Nucleic Acid detection
CURRENT APPLICATION NUMBER: US/09/406, 065
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 09/138, 972
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: 09/252, 436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042, 287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 78
LENGTH: 486
TYPE: DNA
ORGANISM: Pyrococcus furiosus
; US-09-406-065-78

RESULT 13
US-09-406-065-78
; Sequence 78, Application US/09406065
; Patent No. 6312902
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leippe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A
; APPLICANT: Hartnett, James R
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J
; APPLICANT: Welch, Roy
TITLE OF INVENTION: Improved Nucleic Acid detection
FILE REFERENCE: Improved Nucleic Acid detection
CURRENT APPLICATION NUMBER: US/09/406, 065
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 09/138, 972
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: 09/252, 436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042, 287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 78
LENGTH: 486
TYPE: DNA
ORGANISM: Pyrococcus furiosus
; US-09-406-065-78

RESULT 14
US-09-621-976-15639/c
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas, Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins
; FILE REFERENCE: GENSET_054P12
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO: 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-976-554-924
; Sequence 924, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976, 594
; CURRENT FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: 60/240, 409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO: 924
; LENGTH: 2802
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 481118.7
; NAME/KEY: unsure
; LOCATION: 1873, 2029
; OTHER INFORMATION: a, t, c, g, or other
; US-09-976-554-924

Query Match      2.9%;  Score 36.8; DB 4; Length 2802;
Best Local Similarity 47.1%; Pred. No. 0.7; Mismatches 162; Indels 3; Gaps 1;
Matches 147; Conservative 0; MisMatches 162; Del 0; Insert 0;

QY      848 TCTTAACATAGCGCTTCCTGATCANAACAAAGTACATGAGCAATGCTGACTG 907
Db      1006 TGTGAAAGATCGGAGTTGACTATTTAAGTGTGAGCAGCATGATCTATGATA 1065
QY      908 CAACATGTTGTCACAGAAGAGAAGAACCCAAAGCACTGTCGAAGAGGAAGC 967
Db      1066 CAAATAACTTGTAAATAGACAAACCTGGAGAGCTTGTGACTCTCGTGACATT 1125
QY      968 AAAGGCAGCTAGGAGCAGTGGACTCTAGCAGCTGATGTTCCGAAAGGCAC--AAA 1024
Db      1126 ATATGGACAAGAGGAGTTGACAAAGCAATAGAAGATTGTGAGTTGACATTAGAAA 1185
QY      1025 GTATGCTCTGGAGCACAGGCTTACAGAGAGCTAGAGCAAGGAGA 1084
Db      1186 CTGCCCCACTCACAGAAATGCGAGAAATACTCTCTGCGAGACACTTGAGAGGAGG 1245
QY      1085 AGCCTTGACCAAAGGAGAAGAAATGTCAGAAAGGATATCAAGGAGATGAGG 1144
Db      1245 ACAGTTGAGAGAAGAAAGTTTAAATGCTGAAGTTACTATAGAAAGCTTGGC 1305
QY      1145 TGGTGCTAGTC 1156
Db      1306 TTGGATAGAC 1317

; US-09-621-976-15639/c
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas, Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins
; FILE REFERENCE: GENSET_054P12
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO: 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-09-621-976-15639

DB 1757 CTCGGTATACCTAGCTCAGATAAGAACATTATCTCTGA 1796

Query Match Similarity 2.9%; Score 36.6; DB 4; Length 505;
 Best Local Match 13.0%; Pred. No. 0.3; Mismatches 170; Indels 0; Gaps 0;
 Matches 48; Conservative 151; Mismatches 170; Indels 0; Gaps 0;

Search completed: July 7, 2004, 20:22:38
Job time : 127 secs

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GenCore version 5.1.6
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Om nucleic - nucleic search, using SW model

Run on: July 7, 2004, 18:55:30 ; Search time 829 Seconds

{without alignments} 7390.523 Million cell updates/sec

Title: US-09-914-220B-2

Perfect score: 1270

Sequence: 1 gaaaatcgagggttttt.....atgaaagggttacaatta 1270

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpna/us60_new_pub.seq: *

19: /cgn2_6/ptodata/1/pubpna/us60_pubcomb.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 533.4 42.0 1673 13 US-10-424-599-138705 Sequence 138705,

2 510.2 40.2 1699 17 US-10-437-963-82511 Sequence 82511, A

3 486.8 38.3 1432 13 US-10-425-114-26760 Sequence 26760, A

4 36.5 1082 16 US-10-425-1941-19 Sequence 259, A

5 372.2 29.3 902 13 US-10-425-114-2966 Sequence 2966, A

6 298.8 23.5 864 16 US-10-259-1940-584 Sequence 584, A

7 254 20.0 376 12 US-09-732-6278-1173 Sequence 1173, A

8 252 19.8 469 16 US-10-259-194A-460 Sequence 460, A

9 210.4 16.6 1458 13 US-10-424-599-138708 Sequence 138708,

10 204.4 16.1 602 17 US-10-437-963-88914 Sequence 88914, A

11 126.6 10.0 968 9 US-09-770-445-291 Sequence 291, A

12 103.6 8.2 1171 13 US-10-424-114-34960 Sequence 34960, A

13 8.2 2019 16 US-10-310-154-128 Sequence 128, A

RESULT 1
US-10-424-599-138705
; Sequence 138705, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO: 138705
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT:847_96258C.1
; US-10-424-599-138705
Query Match 42.0%; Score 533.4; DB 13; Length 1673;
Best Local Similarity 68.9%; Pred. No. 7e-149; Mismatches 336; Indels 10; Gaps 2;
Matches 765; Conservative 0; Sequence 138705,
Sequence 26760, A
Sequence 259, A
Sequence 2966, A
Sequence 584, A
Sequence 1173, A
Sequence 460, A
Sequence 138708,
Sequence 88914, A
Sequence 291, A
Sequence 34960, A
Sequence 128, A
Sequence 13768, A
Sequence 91131, A
Sequence 17160, A
Sequence 80948, A
Sequence 13415, A
Sequence 23635, A
Sequence 3203, A
Sequence 488, A
Sequence 1703, A
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Sequence 110, A
Sequence 27, A
Sequence 27, A
Sequence 139, A
Sequence 428, A
Sequence 428, A
Sequence 27221, A
Sequence 27220, A
Sequence 18427, A
Sequence 80123, A
Sequence 80948, A
Sequence 9261, A
Sequence 124540, A
Sequence 130000, A
Sequence 4, A
Sequence 81510, A

Db 306 CCCAAAGGTTGATTCGAACTGGTGGGTCTTCATGAGAAGGTCAAGAACAAATCATTA 365 ; APPLICANT: Kovalic, David K.
 Qy 320 GGAAGGTCAACGGTTCAAAACATCCAACTGTTCTACATGCTTGTCACTACAGGGATC 379 ; APPLICANT: Zhou, Yihua
 Db 366 GGAAGGTCAACGGCAAGAACCTTCACAAATTCTCAACTTGCTTCATCACAGGGCTG 425 ; APPLICANT: Cao, Yongwei
 Qy 380 GACCAAACATCGGCACAAATTGAGGATACATGGATGAGGAAACCTTGTATTGATT 439 ; APPLICANT: Mu, Wei
 Db 426 GGCTGAGAAATCACACACAAGTTGAAGCACATGAGCAGGACRAESCCAAATGAGA 485 ; APPLICANT: Boukharov, Andrei A.
 Qy 440 GGTCTCTGGAAAGAGAAMAAAGAACTAGCGGTTAGGCATCGTGTGCTACATGAA 499 ; APPLICANT: Barbausk, Brad
 Db 486 GGTCTCTGGAAAGAGAAGAAAGAAATGCTGAGGATCTGGTGGGATCTGGTGGCAAGATGAA 515 ; APPLICANT: Li, Ping
 Qy 500 GTCTGGTGAACGGTGCCTTGTGCACTTGTGAGGAAAGCACATGAGCAGGACRAESCCAAATGAGA 559 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21 (53221)B
 Db 546 AGCTGGGAAAGGGGGTGTGGCTGGCTGGGGATTTGGATGGAGGAGGAGGAG 605 ; CURRENT APPLICATION NUMBER: US/10/437, 963
 Qy 560 CTTTCTTCCAAATGTTACACTATGCGAGACTGTGTTATGAGTGGAAAGTATGG 619 ; CURRENT FILING DATE: 2003-05-14
 Db 606 CTTCTCTTCCAAATGTTACCAACAGGAGATTAGTTATGAGTGGAGCTGATCG 665 ; NUMBER OF SEQ ID NOS: 204966
 Qy 620 GTTGTGAAACAAGGAGGAAAGCTCCAGTGTATGACTGTAGGAAAGGATGG 679 ; SEQ ID NO: 82511
 Db 666 CTTTGATGAAACAAAGGAGGAAAGCTCCAGTGTATGACTGTGGAGAAAGGATGG 725 ; LENGTH: 1699
 Qy 680 TGCAAGAGAAGAAATGGTGGAAATCTCTTAAAGGGAGAACCTGGAGA 739 ; TYPE: DNA
 Db 726 TGCAGCAGACGGAGAAGATGGATGAAATGCTTGTATCAGGAGAAACATAGGA 785 ; ORGANISM: Oryza sativa
 Qy 740 AGCCATGCAACAGTGTGAAATGGCATACTATGEGGACATTATGTTCACT 799 ; FEATURE:
 Db 786 GGCTATGCAACAGTGTGAAATGGCATACTATGEGGACATTATGTTCACT 845 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_81934C.1
 Qy 800 GТАTGGAACTACGGATTTGGCTTAGGTTAAACCACTCCATCTTAACTAC 859 ; US-10-437-963-82511
 Db 846 CTGCCAAAGGAGCAGAAAGGGGCTCTGGCAGTAAAGATTCATGCCATCTTACATGC 905 ;
 Qy 860 AGCTGCCTCAAACTAAACATACGATACGAGCAATTGGTCACTGCAACATGTGT 919 ;
 Db 906 AGCTGTGTTGATTAAGCTGAACTGCAACGGCTACGAGAAACATGTTACATG 955 ;
 Qy 920 GACAGAGAGAGAAACCCAAAGACACTTCTGAGCAAGGGAAAGCAGGAGCT 979 ;
 Db 966 GGGTAGGGATGAGAACATGTGAAAGCCATTATTAGGGGGTAGGCTAGAGCACT 1025 ;
 Qy 980 AGGAGAGATGACTCTGAGCTGTGATTCGAAAGGCAAAAGTATGCTCTGAGA 1039 ;
 Db 1026 TGGCAACCGATACTGCCAGGGAAAGTTCTAAAGGCAAAATGCCCTCAAGA 1085 ;
 Qy 1040 CAAGGGATTTAGAGGAGGTTCTGAGCACTGAGAGAGAGCTGTACCAA 1099 ;
 Db 1086 CAAGCAATGCTAAAGATGTGAGATGCTGCTGCACTGACAGGCTTACAAA 1145 ;
 Qy 1100 GCAGAGAGAGATGTCACAGGAAATTCAGGGAGAGTGAAGTGGCTAAGTCAA 1159 ;
 Db 1146 GCAGAGAGAGATTAAGGAAATTGGCACTGAGTGTGCTTCTCCGATCT 1205 ;
 Qy 1160 GAGCCTTTTGTTGTTGATGAGTGTGATGGCAATGTTGTTCTCCGATCT 1219 ;
 Db 1206 AA-----ATGGCTCACTATTTGGCTGGGTGCTTCAGPATTCATGGCTGT 1259 ;
 Qy 1220 TCGACCCAGAGAGTTAACCGAGATAATCT 1250 ;
 Db 1260 CACGCTCTAACGCTCAAGGCAATACTT 1290 ;

Query Match 40.2%; Score 510.2; DB 17; Length 1699;
 Best Local Similarity 72.3%; P: 0; Mismatches 28; Indels 1; Gaps 1;
 Matches 676; Conservative 0;

Qy 193 GAGAGGAAATAGTGTACTGAGGAGGAGCCATGCTGAGAGGT 251 ;
 Db 1410 GATATGAGATAACTGTGAGGAGCTCTTGTGCACTGAACTCCGCAAGATGGC 1351 ;
 Qy 252 AATGTTCTCTCAAAGTGTAGTGTAGACTGAGCTGAGGTCTTGTGAGTAACAGC 311 ;
 Db 1350 TCTGCCCCACTGTGGTCTCTAAATGGAGGTCCTCATGACAAGTAAACAA 1291 ;
 Qy 312 ATTATAAGGAAGTCAGGTTCAAAACCATACTCAAGTACTGACTCTTTGTCACT 371 ;
 Db 1290 GTCATCAGAAAGGCCATGCGCAAGAACATCAAGTGTGGACAGCTTGTCACT 1231 ;
 Qy 372 AGGGCATGGACAAACTCGCAGCACAAATTGGGATACATGGCATGAGGCAACT 431 ;
 Db 1230 AGAGCTTGGTCAGGCTCTCTGCAATAATGGAGATACTTGGCAGAACGATCCC 1171 ;
 Qy 432 ATTTAAGGAAGTCAGGTTCAAAACCATACTCAAGTACTGACTCTTTGTCACT 491 ;
 Db 1170 ATTGACTGTAATGGAGAAAGGAAACAAATGCTGGTTAGGCTAGTGGT 1111 ;
 Qy 492 AGCTGAGTCTGGTACGGCTCTGGCTCTGGCTCTGGATTTAGCTATGGAA 551 ;
 Db 1110 AACATGAGAGTGGGGAGCTGTGAGTGTGGCTGGAGCTTGTGGATGGCTATGGAA 1051 ;
 Qy 552 GANGAACTTCTTCCAAATGTCACCTATGCGACTGTGTTATGAGGCGAA 611 ;
 Db 1050 GAAGGGAGCTTCTCATTCCAAATGTCCTCAATGGCAGATCTTGTATGAGTGG 991 ;
 Qy 612 GTATTGGTTGATGAAACAAGGAGGAAAGCTGCGAGTATGACTGTAGGAA 671 ;
 Db 990 CTATTGGTTGATGTCAGAGGAAATTGGATTGGGATGAGTATTCAGAGAAG 931 ;
 Qy 672 AGGATTGGCAGAGGAGAGGAGGAAATTGGATTGGGATGAGTATTCAGAGAAG 731 ;
 Db 930 AGGATTGGCAGAGGAGAGGAGGAAATTGGATTGGGATGAGTATTCAGAGAAG 871 ;
 Qy 732 CTGGAGGAGGCCATGCAACACTATGAAATGCCATACATGCGGAGATTGT 791 ;
 Db 870 TTGAGGAGGCTCATGCAACATATGAAATGGCGATCTACATGGAGATGACTCATG 811 ;
 Qy 792 TTGAGGAGGCTCATGCAACACTATGAAATGCCATACATGCGGAGATTGT 851 ;
 Db 810 TTCAATGTTGGGAAATGAGATATGGCTGCTGAAATCCATGTCATCTC 751 ;
 Qy 852 AACATGAGGCTCATGCAACATATGAAATGGCGATCTACATGGAGATGACTCATG 911 ;
 Db 750 AACATGAGGCTCATGCAACATATGAAATGGCGATCTACATGGAGATGACTCATG 691 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.

RESULT 2

US 10-437-963-82511/C

; Sequence 82511, Application US/10437963

; Publication No. US20040123343A1

; APPLICANT: La Rosa, Thomas J.

QY 912 ATGGTGTGACAGAAGAGGAAACCCAAAGCAAGCACTTCATGAGAGGGAAAG 971
Db 690 ATGGTGTGCGAGGATGAAACATGTTGAAGCATGTCAGCAGGAAAGCAAGA 631
QY 972 GCAGAGCTAGACAGATGGACTCGACCGTATGATTCCGAAGGCACAAGTATCT 1031
Db 630 GCTGACTTGTGACAGAAGATCAGCGAGGGACTTCTGAAAGGCCAGAACATTCC 571
QY 1032 CCTGAGCAGAAGGGATTAGAAGAGCAGTGAGGACACTTGCAAGCAAGAAAGCCTG 1091
Db 570 CCAGAGACAGAGATCCAGCGTGTGACTTCGGGACAGGATAAGCTG 511
QY 1092 TACCAAGGAGAAGAATGTACAAAGGATATT 1126
Db 510 TACCAAAACAGAAGGAGCTGTACAAAGGCTCT 476

RESULT 3
US-10-425-114-26760
; Sequence 26760, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Koralic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26760
; LENGTH: 1432
; TYPE: DNA
; ORGANISM: Zea mays -
; OTHER INFORMATION: Clone ID: LIB4574-008-F5_FLI
; US-10-425-114-26760
Query Match 38.3%; Score 486.8; DB 13; Length 1432;
Best Local Similarity 71.7%; Pred. No. 6.3e-135; Mismatches 638; Conservative 0; Indels 0; Gaps 0;
Matches 638; APPLICANT: Lange, Markus B.
QY 237 CCACCTCAGAGGGATAATGTTCTCTTAAGTTGATAGTGAACTGAGCTCTTGATGAG 296
Db 233 CCTCCCGAGGATGGCGGCCAACCGTGTCTCTCATGAGGCCCTCACAC 292
QY 297 AAAGTCAGTGTAGAGATATAAGGAAGTCACGGTCCAAACCATCCAGACTCTACA 356
Db 293 AAGGTTAAGAGCAATCATCAAAGAACGGCATGGCGAACCGCTGAGTRGCGAGC 352
QY 357 TGCCTTGTGACTACAGGGATGCCAAACACTCGAGCACAAITGGATACATGG 416
Db 353 TGCTTGTGACTATAGACCATGGTCAGGTACATGCCATAATTGGATACCTGG 412
QY 417 CATGAGCAGACATTGATGGTCTTGGAAAGAGAACAAAGAACATGGCGTTA 476
Db 413 CAAGGACACATCCATTGAACTGACTTGAGAACAAATGTCCTGTTA 472
QY 477 GGCATCGGTTGTGTGACTCTGTTGAGCTGCGCTTGAGCTGTGCGTGGAA 536
Db 473 GGCACTGGTTGGCAGCATGAAAGCGGGAGGCTGATGTGTCGGGAG 532
QY 537 TTAGCTTATGGAAAGAGGAAACTTCTTCCAACTTCCACCTTGGCAGACTG 596
Db 533 CTAGCTATGGCAAGAAGGAGTTTCATCCAAATGTCCTCCATGGTGGAC 592
QY 597 TTATGAGGTGGAGTTGTTGAGGAAACAAGGAGAAAAGCTCGAGTAT 656
Db 593 GTTATGAGGTGAACTCATGGATTGAGATGTTAAGAGGAAATCCGAGTGA 652

RESULT 4
US-10-559-194A-19
; Sequence 19, Application US/10259194A
; Publication No. US2004001081A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Majid P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provert, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhou, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259-194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SEQ ID NO 19
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-10-259-194A-19
Query Match 36.5%; Score 463.8; DB 16; Length 1082;
Best Local Similarity 72.0%; Pred. No. 4.3e-128; Mismatches 675; Conservative 0; Indels 10; Gaps 5;

Publication No. US20040010815A1
 GENERAL INFORMATION:
 APPLICANT: Lange, Markus B.
 APPLICANT: Ghassemian, Majid
 APPLICANT: Briggs, Steven P.
 APPLICANT: Cooper, Bret
 APPLICANT: Glazebrook, Jane
 APPLICANT: Goff, Stephen A.
 APPLICANT: Katagiri, Fumiyaaki
 APPLICANT: Kreps, Joel
 APPLICANT: Moughamer, Todd
 APPLICANT: Provart, Nicholas
 APPLICANT: Riche, Darrell
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
 FILE REFERENCE: 70029-NP
 CURRENT APPLICATION NUMBER: US/10/259,194A
 CURRENT FILING DATE: 2003-01-07
 PRIOR APPLICATION NUMBER: US 60/325, 277
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: US 60/370, 743
 PRIOR FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: US 60/370, 620
 PRIOR FILING DATE: 2002-04-04
 NUMBER OF SEQ ID NOS: 662
 SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
 SEQ ID NO: 584
 LENGTH: 864
 TYPE: DNA
 SOURCE: Triticum aestivum
 S-10-259-194A-584

Query Match 23.5%; Score 298.8; DB 16; Length 864;
 Best Local Similarity 73.4%; Pred. No. 1.3e-78;
 Matches 395; Conservative 0; Mismatches 142; Indels 1; Gaps 1;

Matches 395; Conservative 0; Mismatches 142; Indels 1; Gaps 1;

589 CAGACTGTTATATGAGGTGGAAAGTATTGGTTATGAAACAAAGAGGAAARGCTC 648
 1 CAGACCTATATGAGGTGGAAACTCTT-GTTTGATGCTTAAGGGAAAGCTC 59

649 GCAGCTGATACTGAGGAGAACGATTGGCGCCAGCAGAAGAAATGGTGGGA 708
 60 GTAGTCACATGAGGAGAGGATGGAGCAGGGATAGGGCA 119

709 ATTCTCTTTAAGGAGGAGAACCTGGAGGCATGACAGTATGAAATGGCATAG 768
 120 ACGATCTTAAAGGAGGAAATTGGAGGGCTATGCCAAATGAGTGGCTG 179

769 CATACTGGGAGCATTTATGTTAGCTGATGTTGAGGAAGTACCGATAATGCTTAG 828
 180 CGTATATGGAGATGATTCAGTTCAAGTGTGTTGGAAACTACAGAGATATGGCTTGG 239

829 CAGTAAACCCATCCATTAACATACAGCTGGCTCATCAACTAACGATAC 888
 240 CTGTGAAACCCGTCATCTAACATGCTGCTGCTGATCACAAACAGATATG 299

889 ATGAAGCCATTGGTCACTGCACATGGTGTGACAGAGAGAAAACCAAAGCAC 948
 300 ACGAACGCTATCCACAGCTGGTACATGTCGCTCAAGGAGAACACACTGAAANGGCC 359

949 TGTTCAGAGAGGAGAGCAAGGAGCTAGGAGAGATGCACTCAGCACGGTGTATT 1008
 360 TGTTCAAGCTGGAAAGACGTAGAGCCAGCTGGCCAGACAGAAATGAGGGAGACT 419

1009 TCCGAAGGACAAGATGCTCTGAGCAAGGGGATTAGAAGAGGACTACGAGCAC 1068
 420 TCCTGAAAGCCAGAGAACACTCCCGGAGACAAGGAGATCATGGGGAGCTCGTCG 479

1069 TTGCAAGCAAGAGAAGACCTGACCCAAAGCAGAGAAATGTTGAAAGGAATT 1126
 480 TGGCGGAGACAGATAAGCAGTGTACCCAGAGCAGGGAGCTATGAGAGCTG 537

RESULT 8
 US-10-259-194A-460/C
 ; Sequence 460, Application US/10259194A
 ; Publication No. US20040010815A1
 GENERAL INFORMATION:
 APPLICANT: Lange, Markus B.
 APPLICANT: Ghassemian, Majid
 APPLICANT: Briggs, Steven P.
 APPLICANT: Cooper, Bret
 APPLICANT: Glazebrook, Jane
 APPLICANT: Goff, Stephen A.
 APPLICANT: Katagiri, Fumiyaaki
 APPLICANT: Kreps, Joel
 APPLICANT: Moughamer, Todd
 APPLICANT: Provart, Nicholas
 APPLICANT: Riche, Darrell
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 CURRENT APPLICATION NUMBER: US/09/732,627A
 CURRENT FILING DATE: 2000-12-08
 NUMBER OF SEQ ID NOS: 4930
 SEQ ID NO: 1173
 LENGTH: 376
 TYPE: DNA
 ORGANISM: Gossypium hirsutum
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(376)
 OTHER INFORMATION: unsure at all n locations
 OTHER INFORMATION: Clone ID: LIB3493-057-P1-M1-C7
 US-09-732-627A-1173

Query Match 20.0%; Score 254; DB 12; Length 376;
 Best Local Similarity 80.4%; Pred. No. 2.2e-65; Matches 296; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Db Qy 462 GAACTAGCCGGTTTACCCATGGCGTGTGAGCTGAGCTGGCGCTGTC 521
 Db Qy 522 CATTGCGCTGGATTAGCTTATGGGAAGAGAAACATTCTTCCCAATGTCCA 581
 Db Qy 68 CATGTCGGCTGGAAATGGTTAGGTATGGAAAGAACAGCTTCTCCAAACGTCCA 127

Db Qy 582 CCTATGCCAGCTTGTGTTATGAGGTTGGCTGTCAGTTGAAATCANGNAACTGCTTGTGA 67

Db Qy 8 GRATACTCTTTGGTGTGGCTGTCAGTTGAAATCANGNAACTGCTTGTGA 67

Db Qy 128 CCAATGGCAGACATAATTATGAGGAGCTTGGGAAAGGAAAGCT 187

Db Qy 642 AAAGCTGCGACTGATGACTGTGAGGAAAGGATGGCTGAGCAGAGAAATG 701

Db Qy 188 AGCTGGCTGATGACTGTGAGGAAAGGATGGCTGAGCAGAGAAATG 247

Db Qy 702 GATGGAAATCTCTTTAAGGAGGAAACTGGAGGAGCCATCAACAGTATGAAATG 761

Db Qy 248 GACGGAATCTCTTATTCAAGGAGAAATGACTAACAGGAGCCATGAACTGATGAAATG 307

Db Qy 762 GCGATGCAATACGGAGGAAATTGATGTTGGCTGAGCAGAGAAATG 821

Db Qy 308 GCGATGCGTACATGGTGTGACTGTTGGAGGAGCTTGGGAAAGTGGAGACATG 367

Db Qy 822 GCTTGTAGC 829

Db Qy 368 GCTTGTAGC 375

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70039-NP
CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIORITY APPLICATION NUMBER: US 60/325,277
PRIORITY FILING DATE: 2002-04-04
PRIORITY APPLICATION NUMBER: US 60/370,620
PRIORITY FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
SEQ_ID NO: 460
LENGTH: 469
TYPE: DNA
ORGANISM: Musa acuminata
FEATURE:
NAME/KEY: misc feature
LOCATION: (251)..(251)
OTHER INFORMATION: n = any nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (352)..(352)
OTHER INFORMATION: n = any nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (383)..(383)
FEATURE:
NAME/KEY: misc feature
LOCATION: (437)..(437)
OTHER INFORMATION: n = any nucleotide
; US-10-259-194A-460

Query Match 19.8%; Score 252; DB 16; Length 469;
Best Local Similarity 72.1%; Pred. No. 1e-64;
Matches 338; Conservative 0; Mismatches 130; Indels 1; Gaps 1;

QY CCACTCAAGAGGCTTAATCTCCCTCTAAAGTGTAGTGAACTGGATCTGGATCG 296
Db 469 CCTGCCAACAGTGAATAGTTACCAAGTNGAGTCAGAGTGGGTCTCATAG 410
Qy 297 AAGCTCAGTAAAGCATTATAAGGAAAGTCAACGTTCAAACATCCAGTCTACA 356
Db 409 AAAGCAAAAGCAATTATAA-GAANGCCATGTCAAACACNCAAAATGTCANT 351
Qy 357 TGCCTTGTCACTACAGGGATGGCACCACAAACTCGCACACAAATTGGATCATGG 416
Db 350 TGCTCTGAAATTAGGCTATGGTTAAAGACTTCACACAAAGTGTGAGATCTGG 291
Qy 417 CATAGCAGCAACCTTAACTGGATGGAAAGGAAAGAAGCTAGCGGTTMA 476
Db 290 CAAGGAGCAGGACCATGAACTTATAGGGAAAGAANAGGAGAGTGGTGTG 231
Qy 477 GGCATCGGTGTGTAGCATGAACTCTGGTGAAGCTGGCCTTGCGATGTGCTGGAA 536
Db 230 GCAATCGGCTGTGTAGCATGAGGAGCTGGCACTCTTCATGTGGGTGGAA 171
Qy 537 TTAGTTATGGAAAGGAAACTTCTTCCCAATGTTCACTTAACTGGAGACTG 596
Db 170 CTGGCTAGGAAAGAAGGAATTTTCAACGTCCTCCATGGGAGACCT 111
Qy 597 TATATGAGGTGTGAACTTATGGCTATGAAACAGGAGGAAAGCTGGTCA 656
Db 110 GTTATGAGGTGTGAACTTATGGCTATGAAACAGGAGGAAAGGAGGAGTGGAC 51
Qy 657 ATGACTGTAGGAAAGGATTTGGTCAGGAGCAAGAGAAAGAATGGTGG 705
Db 50 ATGACAGTAGGAGAGGATTGAAGCTGCCAAAAGAAGAAAGGGTGGAAAG 2

RESULT 9
US-10-424-599-138708
; Sequence 138708, Application US/10424599
; Publication No. US20040031072A1
GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ_ID NO 138708
LENGTH: 1458
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1458)
OTHER INFORMATION: unsure at all n locations
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1458)
OTHER INFORMATION: Clone ID: PAT_MRT3847_96260C.1
; US-10-424-599-138708

Query Match 16.6%; Score 210.4; DB 13; Length 1458;
Best Local Similarity 68.3%; Pred. No. 6 6e-52;
Matches 362; Conservative 0; Mismatches 91; Indels 77; Gaps 2;

Qy 515 GCTGTGCGATGTTGGCTGGATTAGCTTATGGAAAGGAAGAACCTTCTTCCAA 574
Db 96 GTRGGCTGCTGGCTGGCTGGATTAGSATATGGAGAGGAAAGCTCTCTTCCAA 155
Db 36 GAGAAGAAATCACTGGTGGCTGGCATGGGAGCATGAAGCATGAAGCTGGGGAGCTGC 95
Qy 515 GCTGTGCGATGTTGGCTGGATTAGCTTATGGAAAGGAAGAACCTTCTTCCAA 574
Db 96 GTRGGCTGCTGGCTGGCTGGATTAGSATATGGAGAGGAAAGCTCTCTTCCAA 155
Db 36 GAGAAGAAATCACTGGTGGCTGGCATGGGAGCATGAAGCATGAAGCTGGGGAGCTGC 95
Qy 575 TGTCCACCTATGGCACACTGTGATATGAGGGAGATTGGTTGATGAACAAA 634
Db 156 TGTCCACCAAGGCAGGATTTAGTTATGAACTGTGACTCATGGCTTGTGAACAAA 215
Qy 635 GG-----
Db 216 AGAGTAAGTGGCATTAATTATGGATGGCTGTGGACTGTGCTATAGGACC 275
Qy 637 -----AGGAAAGACTCTCAGTGTATGACTGTGAGGAAAGCTGGTGCACAG 687
Db 276 TGATTTCAACAGGGAAAGCTCGCAGTGTATGACTGTGAGGAAAGATGGTGCACAG 335
Qy 688 ACAGAAGAAATGGATGGAAATCTCTTTRAGGAGGAAACTGGAGGAGGCCATGC 747
Db 336 ACGGGAGAAGGAGTGGATGAAATGCTTGTATGAGGAAAGACTGAGGGCTATGC 395
Qy 748 AACGATGAAATGGCCATAGCATACATGGGAGCAGTTTATGTTGAGCTGTATGGA 807
Db 396 AAGA-----GCATGTGATATGGAGAGTACTCTGTCAGTGTGCTGGAA 445
Qy 808 ACTACCGAGATGGCTTGTAGCATGTTAAACCCATGCCATCTTAACATGAGCTGTGCC 867
Db 446 AGTATGAGATATGGCTGTGGAGTAAAGAATCATGCATCTTAACATGGAGGCCATGT 505
Qy 868 TCTCAACTAAAGCTAGTGTGAAAGCTGGTCACTGTCAGTGTGCTGG 917
Db 506 TGATTAAGCTGACCGCTACGAGAAGCCATAGGACATGAGCATGTGCTGG 555
; Sequence 88914, Application US/10437963
RESULT 10
US-10-37-963-88914

; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5321)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 88914
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Oryza sativa
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8771C.1
; US-10-437-963-88914

Query Match 16.1%; Score 204.4; DB 17; Length 602;
Best Local Similarity 65.6%; Pred. No. 2.4e-50; Mismatches 156; Indels 0; Gaps 0;
Matches 298; Conservative 0; MisMatches 156; Indels 0; Gaps 0;

Qy 199 GAATAGTAGTACTGAGGAAGTGCGCTTGCGATAGTGCCACATCGAAGGGPATGTC 258
Db 149 GAGATPACGGGGATAAACTCTCTGTGCGCACTGAACCTCCITGAGATGGCTGTC 208
Qy 259 CTCTTAAGTGTAGTGTAGCTGGATGAGCTGGCTTGTGACTACAGGGAT 318
Db 209 CACCCTGGTACCTCTGATATGGAGGCCTTAATGATAAGCCAGAAGCAGGCTCA 268
Qy 319 AGGAAGTCCAGGTTCCAAACCATCGAACAGTCTACACTCTACATGCTTGTGACTACAGGGAT 378
Db 269 AGGATGCGCTGTGCGAGAAACCTCAAGSTTGTGACACATGCTTGTGCTACTACAC 328
Qy 379 GGACCAAACACTCGCAGCACAAATTGAGGATACATGGCATGAGCAGCACATTGAT 438
Db 329 GGGTCAGGTTCTCGACAAATTCGAGGATCTGGAGAAGACAGGATGATCGAC 388
Qy 439 TGGTCTCTGGAAAGAGAAAAGACTAGGCCSATTGACCATCGGTTGTGCTAGCTGA 498
Db 389 TAGTACTGGAAACAGAAAGAGAACCTGACTGCTTACGCTTGTGCAACTAACATGA 448
Qy 499 AGTCGGTGAACGTCGCTTGTGCAATGTTGCTGGAAATTAGCTTATGGAAAGAGGA 558
Db 449 AAAGAGGSGCGCGTGTGATTTGTTACATGGTAACTCGGAGCTTGCTATGTAAAGAA 508
Qy 559 ACTTTCTTTCACATGTCTCCACCTATGGCAGACTGTGTTATAGGCTGAAGTTATG 618
Db 509 GCTTTTATTCACATGTCTCCACATGGCAGACTGTGTTATAGGCTGAAGTTATG 568
Qy 619 GGTGTTGATGAAACAAAGGGGAAAGCTGGCAGCTGTATGAACTGGAACATG 652
Db 569 GGCTTGATGATGTCACAGAGGGAAAGCCGGAAG 602

RESULT 11
US-09-770-445-291
; Sequence 34960, Application US/10/425114
; Publication No. US2004034888A1
; General Information:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 34960
; LENGTH: 1171
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017365D08_PLI
; US-10-425-114-34960

RESULT 12
US-10-425-114-34960
; Sequence 34960, Application US/10/425114
; Publication No. US2004034888A1
; General Information:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 34960
; LENGTH: 1171
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017365D08_PLI
; US-10-425-114-34960

| Query Match | 8.2%; Score 103.6; DB 13; Length 117; | Best Local Similarity 48.8%; Pred. No. 6; 9e-20; Matches 410; Conservative 0; Mismatches 409; Indels 21; Gaps 4; |
|--|--|--|
| Qy | 291 GATGAGAACTGCAATTCTTACAGGATTAAGGGAGGTCACGGTCCAAACCATCCACTAC 350 | APPLICANT: Banu, G. |
| Db | 44 GATAAGAAATCTTACAGGATTAAGGGAGGTCACGGTCCAAACCATCCACTAC 103 | APPLICANT: Bell, Erin |
| Qy | 351 TCTACATGCTTGTCACTACAGGGATGGACCAAACCTCCAGACAATTGAGGAT 410 | APPLICANT: Bodduvalli, Raghava |
| Db | 104 GGTGCTGTTGTGAAGTCAAATTATCGGAAGCTCTGGATGCCGGTGTACAAAG 163 | APPLICANT: Deikman, Jill |
| Qy | 411 AGATGGATGAGGAGGACACTATGAAATTGGAATGGCTTCTGGAAAGAGAAAAGACTAGCC 470 | APPLICANT: Deng, Molian |
| Db | 164 AAGGGGATGAGGAGGACACTATGAAATTGGAATGGCTTCTGGAAAGAGAAAAGACTAGCC 103 | APPLICANT: Dong, Jinzhuo |
| Qy | 471 GGTGTTACCATCGTGTGCTGTTGACATGAGAAGGGGGGGTCTGTGACAATTCT 280 | APPLICANT: Duff, Stephen M. |
| Db | 221 GGTGTTACCATCGTGTGCTGTTGACATGAGAAGGGGGGGTCTGTGACAATTCT 280 | APPLICANT: Galligan, Meghan M. |
| Qy | 531 TGGGAAATTAGCTTATGGG--AAAGAGGAACCTTCTTCCAAATGTCACCTATG 587 | APPLICANT: Hinckley, Brenda S. |
| Db | 281 CCTGAAATATGCAATTGCTGTTCAACTGAGTCAGCAGGAACTCTGCTGTTCCACCTAAC 340 | APPLICANT: Huang, Shishien |
| Qy | 588 GCAGACGTGTTATGAGGGGAGGTTATGGGTTGATGAAACALAGGGAAAGCT 647 | APPLICANT: Johnson, G. Richard |
| Db | 341 AGCAGACTAAATATGAGGTGACTTGTGTTGAAAGGAGGAGGAGGAGGAGGAGGAGG 395 | APPLICANT: Kretzmer, Keith A. |
| Qy | 648 CGCAGCTGTTATGAGGGGAGGTTATGGGTTGATGAAACALAGGGAAAGCT 647 | APPLICANT: Jung, Vincent |
| Db | 396 ---GGGACTGACAACTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 451 | APPLICANT: Kacetti, Lucille B. |
| Qy | 708 ATTCTCTTTAGGAGGAACCTGGAGGACATGCAGCAACATGAAATGGCATA 767 | APPLICANT: Lee, Chao-Qiang |
| Db | 452 AATGCAATTGCTGTTCAATTGCTGAGCTTCCAAAGCGGATATGAGGCTGCC 511 | APPLICANT: Li, Jie-Yi |
| Qy | 768 GCATACATGGGGAGGTTATGGGAGTACCGGATATGGCTTA 827 | APPLICANT: Liu, Jingdong |
| Db | 512 AAGTACATTGAGTACAGACTGTTGTTGAGATGAGAAGGAGGAGGAGGAGG 565 | APPLICANT: Luu, Bin |
| Qy | 828 GCGTAAACCCATCCATTAACATAGCTGCTGCTCATCAACTAACGATAC 887 | APPLICANT: Luetky, Michael M. |
| Db | 566 CAACTGAGATAGCTGAACTAACATGCTGCTGCTGCTCAACTAGTGTGAGGATTAC 625 | APPLICANT: Lund, Adrian |
| Qy | 888 GATGAGCAATTGCTACTGCAACATGCTGAGACAGAGAGAAAACCCAAAGCA 947 | APPLICANT: Madison, Linda L. |
| Db | 626 AAGGAACCTGCGAAGCTTGCACCAAGCTTCTGAGATAGACGCAAAATGTCAGAGCT 685 | APPLICANT: Malloy, Kathleen A. |
| Qy | 948 CGTTCTAGAGAGGGAAAGCAAGGGAGAGCTGAGCTGAGATGGAGACTACAGCACTGATG 1007 | APPLICANT: McKiel, Christine L. |
| Db | 686 CTCTACAGGAGGGTCAGCTTACATCACTGAGCTGAGCTGAGGGCAT 745 | APPLICANT: Miller, Philip W. |
| Qy | 1008 TCCCGAAGGCAAAAGTATGCTCTGAGCAAGGGGATGAGAAGAGAGTACAGCA 1067 | APPLICANT: Padmavathi, Manchikanti |
| Db | 746 ATCACAAAGGCACTGGAAATCTGCTCACACAGGAGGTGCAAGTGGATAATAAGTC 805 | APPLICANT: Parnell, Laurence D. |
| RESULT 13 | US 10-310-154-128 | APPLICANT: Peart, William G. |
| Qy | 1068 CTGCGAGGAGAGAGCCCTGTCACAAAGCGAAAGAAATGCAAGGAATTTC 1127 | APPLICANT: Teunissen, Dan |
| Db | 806 CTGCAAGGAGAGATCAAGGATCACAGAGAACGCCAAATTCTACAGCACATGTC 865 | APPLICANT: Vidy, K.R. |
| Query Match | 8.2%; Score 103.6; DB 16; Length 2019; | APPLICANT: Xin, Zhanguo |
| Best Local Similarity 48.8%; Pred. No. 9; 8e-20; Matches 410; Conservative 0; Mismatches 409; Indels 21; Gaps 4; | APPLICANT: Xu, Nanfei | |
| Matches 410; Conservative 0; Mismatches 409; Indels 21; Gaps 4; | APPLICANT: Yang, Chunzhi | |
| Qy | 291 GATGAGAACTGCAATTCTTACAGGATTAAGGGAGGTCACGGTCCAAACCATCCACTAC 350 | APPLICANT: Zhang, Xiaoping |
| Db | 921 GATAAGAAATCTTACAGGATTAAGGGAGGTCACGGTCCAAACCATCCACTAC 980 | APPLICANT: Zhao, Yajuan |
| Qy | 351 TCTACATGCTTGTCACTACAGGGCATGACCAAACCTCCAGCAAACTTGAGGAT 410 | APPLICANT: Title of Invention: Gene Sequences and Uses Thereof in Plants |
| Db | 981 GGTGCTGTTGAGTCACAAATTATCGGAAGACCTCAGGATGGCGGTGTTACAAG 1040 | FILE REFERENCE: 3B-15(52796)B |
| Qy | 411 ACATGGCATGACGAGCAACCTATGAGATGGCTCTGGAAAGAGAAAAAGACTAGCC 470 | CURRENT APPLICATION NUMBER: US/10/310,154 |
| Db | 1041 AAGGGGATGACGAGGCAATTCAAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGG 1097 | CURRENT FILING DATE: 2002-12-04 |
| Qy | 471 GGTGTTACCATGGGGGGTCTGTGAGTGGCTGAGCTGAGGAGGAGGAGGAGGAGG 530 | PRIOR APPLICATION NUMBER: 60/337,358 |
| Qy | 1068 CTGCGAGGAGAGAGCCCTGTCACAAAGCGAAAGAAATGCAAGGAATTTC 1127 | PRIOR FILING DATE: 2001-12-04 |
| Db | 806 CTGCAAGGAGAGATCAAGGATCACAGAGAACGCCAAATTCTACAGCACATGTC 865 | NUMBER OF SEQ ID NOS: 736 |
| SEQ ID NO 128 | SEQUENCE ID: 128 | SEQUENCE ID NO 128 |
| LENGTH: 2019 | LENGTH: 2019 | LENGTH: 2019 |
| TYPE: DNA | TYPE: DNA | TYPE: DNA |
| ORGANISM: Zea mays | ORGANISM: Zea mays | ORGANISM: Zea mays |
| FEATURE: CDS | FEATURE: CDS | FEATURE: CDS |
| NAME/KEY: CDS | NAME/KEY: CDS | NAME/KEY: CDS |
| LOCATION: (99)..(1757) | LOCATION: (99)..(1757) | LOCATION: (99)..(1757) |
| OTHER INFORMATION: | OTHER INFORMATION: | OTHER INFORMATION: |
| US-10-310-154-128 | US-10-310-154-128 | US-10-310-154-128 |

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Db 1098 GGTCTGTGTCGGTGTGAACATGAGAAGGGCGAGGTGCTCTGCACAACTCT 1157
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Db 1158 CCTGATATGATCATTGTTAACAGTCAAAAGGAGTCTGTTGCTAC 1217
Qy 588 GCAGACTGTATAATGAGGTGAAAGTTGGGTTGATGAAACAAGGAGGGAAAGCT 647
Db 1218 AGCACAGTAAATATGAGCTTACAGTCAAAAGGAGGAGGAGGAGGAGGAGG 648
Qy 648 CGCAGTGATGATGAGTGTAGAGGAAGGATTTGGGTTGATGAAACAAGGAGGGAAAGCT 707
Db 1273 ---GGGACTTGACATGAGAAGAGATGAGCTGAGCTGTTGAGGAGGAGGAGG 1328
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Db 1329 AATGCATGTTCAATCGGGCAAAATATGCTAGACTCTTCAGAGGATATGAGGCTCC 1388
Qy 768 GCATACATGGGGAGGTTTAATGTTCACTGAGTGTAGGAAAGGAGGAGGAGGAGG 827
Qy 1389 AAGTCACTGAGTGTAGACACTTCTTCAGTAGAGGAGGAGGAGGAGGAGG 1389
Db 828 GCAGTTAAACCATGCCATCTAACATGAGCACTTCTCAAACTAAACGATAC 887
Db 1443 CAACTGAACTGAGTCACTGCCAACTTAAACATGCTCCCTGAAACIGAAGTTGAGGATTAC 1502
Qy 888 GATGAGCAATTGTCACPGCACATTGTTGACAGAGGAGGAAACCAACGCA 947
Db 1503 AAGGAGAGCTCGAAAGCTTTCACCAAGGGTCTGAGACTAGACGCCAAATGTCAGCT 1562
Qy 948 CTGTCAGAGAGGGAAAGCAAGAACGGCAGAGCTAGAGGACTCACCGCTGATAT 1007
Db 1563 CTCTACAGGGGTCAGCTTACATGAGCTGAGCTGAGCTGAGGCGAT 1622
Qy 1008 TTGGAAAGGCAAAAGATGATGCTGAGGACAGGCAATTAGAGAGGAGCTACAGCA 1067
Db 1623 ATCAAAGGCACTGAAATCTGATCTGACAAACGAGAAGAAATGACAAAGGATATC 1682
Qy 1068 CTTCAGAGGCAAGAGAACCTCTGACCAAAACGAGAAGAAATGACAAAGGATATC 1127
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RESULT 14

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US-10-25-114-13768
; Sequence 13768, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 3B-21-(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 7128
; SEQ ID NO 13768
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-040-E3_FLI
; US-10-425-114-13768

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Query Match 8.1%; Score 102.8; DB 13; Length 1617;
 Best Local Similarity 50.9%; Pred. No. 1.5e-19;
 Matches 329; Conservative 0; Mismatches 302; Indels 15; Gaps 3;

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Qy 402 TTGAGGATACATGCGATGAGCAACCTATTGAAATTGGTCITGGAAAAGGAAMA 461

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Db 608 TTGTAAGAAGGGCATGATGCTGAGAGCCATTGTCAGACAGATGAGGAGCAG 667
Qy 462 GAACTASCGGTTTACGCATCGCTGTTGCTAGATGAGTCGGTACGTCGGCTGTG 521
Db 668 GTTATTGAGGTTGCGATACAGGTTGTTATATGAGAAGGAGGAGGAGGAGG 727
Qy 522 CATGTTGCTGGGAATTGCTPATGG--GAAAGAGAAACCTTCTTCCAAAGTT 578
Db 728 AGATGTTACCTGAGACAGCATTTGGATCTGAGAAACAATCAAGTCCTGCTACTGTT 787
Qy 579 CCACCTTGCGAGACTTATGAGCTGGAGTTTGCGTTGATGAAACAAGGAG 638
Db 778 CCTCTTAATTCTACCGCTGTGTTGAGATGTTGGAGCTTCTTCCAAAGTT 841
Qy 639 GGAAGAGCTCGAGTGTGATGAGCTGTTGAGGAAAGGTTGGCCAGGAGAAGAA 698
Db 902 GATGAAAGGAAATGTGCTTCAGATGGCAGTATTGAGAAGTTGAGCAGATGAG 961
Qy 842 AAGAACCTGGACTTGACGCCAAATGTCAGCT 901
Db 759 ATGGCCATAGCTACATGGGAGCATTTAGTTGCTGAGCTATGCGAAACTTACAGGAT 818
Db 962 AAGGCTGAAATACATGAGTGTAGCTGAGCTGAGCTTCTTCAAGACT 1021
Qy 819 ATGGCTTGTGAGCTTAAACCATGCGATCTTAACATGAGCTGAGCTTCTTCATCAAGTA 878
Db 1072 AAAGCTCTG-----AAAGTCACTTCAAGCTCAACTGAGCTGCTGAGCTGAGAATG 1075
Qy 879 AAACGATAGCATGAGGATGGTCACTGCAACATTGTTGAGAGAGAAAC 938
Db 1076 AAGAAATACAGAGGAGGAGAAGAACATTGCAAAAGGTTCTGAGACTGAGGAGCAAT 1135
Qy 939 CCAAAGGACTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 998
Db 1136 GTRHAGGCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1195
Qy 999 CGTCATGATTTGCGAAAGGCCAAAGATGCTCTGAGCAGAGCTGAGGAGTCACTGCA 1044
Db 1196 GACTTGAGTGTGAGAAGGAGCACTGAGAATTGATCTCTGATACAGG 1241

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RESULT 15

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US-10-24-599-31694
; Sequence 31694, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 3B-21-(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 31694
; LENGTH: 2568
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(2568)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_128624C.1
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Query Match 7.6%; Score 96.6; DB 13; Length 2568;
 Best Local Similarity 49.4%; Pred. No. 1.4e-17;

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| Qy | 449 AAAGAGAAAGAAGRACTGCCGTTACCATGGCTGGCTAGCATGAAGCTGGAA | | | | 508 |
| Db | 1183 AGATGAGGAGAACAGTGTGATGGACTGTAGAGCTGTATTGAGATGAAGAGGTGA | | | | 1242 |
| Qy | 509 ACGTCGCTTGTCATGTGCTGGATAATTGCTATGG--GAAGANGGAACCTTC | | | | 565 |
| Db | 1243 GGTGCACTGTGACCATTCGACCTGAAATPGCTTGGTGTACAGAGTCCAGCAGGA | | | | 1302 |
| Qy | 566 TTTTCCAATGTCACCTATGGCAGACTGTATATGAGGTGAGGTATGGTTGA | | | | 625 |
| Db | 1303 GTGCCTGTTCTTCACTCACTGTATTGAGTGGCTAGCTTGTGAGTCATTTGA | | | | 1362 |
| Qy | 626 TGAACACAAGGAGGAAAGCTCGAGCTATGACTGTAAGAAGGATGGCGAC | | | | 685 |
| Db | 1363 GAAAGAGAAAGGAG-----TCTGGGATTGACATGAGAAGAAACTTGAGCTGC | | | | 1413 |
| Qy | 686 AGACAGAAGAAATGGATGGAAATCTCTTTAAGGGAGAACCTGGAGAACCCAT | | | | 745 |
| Db | 1414 TGGTAGAGAAGAAAGAGAAGGAAATGGTTAAAGCTGTTAGCATGCAAGAGCTC | | | | 1473 |
| Qy | 746 GCAACAGTATGAAATGCCATAGCATACAGTGGGGACGATTIAATGTTAGCTAGCTG | | | | 805 |
| Db | 1474 CAAAGATATGAAAGGCTGTAAGTACATAGAATATGATCTCTCATGGTGGAGGA | | | | 1533 |
| Qy | 806 GAAGTACCGAGTATGGCTTACAGGTTAAAACCATGCCATTTAACATACAGCTG | | | | 865 |
| Db | 1534 GAAAAGCAGCCAGACCTTGAAGGTT-----GCCCTGCAATTAAAGATGCTGCTG | | | | 1587 |
| Qy | 866 CCTCATCAAATAAAGATACGATGAGCAATGGTCACTGCACATTTGGTACAGA | | | | 925 |
| Db | 1588 CAAGTTGAACTTAAAGACTACAGGAAGAAATTTGTTACAGGTTAGACCT | | | | 1647 |
| Qy | 926 AGAAGAGAAACCCAAAGACCTTCAGAGAGGGGAAGCAAGGAGCTAGGACA | | | | 985 |
| Db | 1648 CGAGGTACATGTTAACCCCTTATAGAAGGGCCAGCATATATGCAAGTAACTGA | | | | 1707 |
| Qy | 986 GATGGACTCGCACCTGATATTTCGAAGGGCAAAAGATATGCTCTGGACCAAGGC | | | | 1045 |
| Db | 1708 CTGGATTGCTGACTTCATTAAGAAGCTTGTGAGATGACCTAACACAGGCA | | | | 1767 |
| Qy | 1046 GATTTGAGGACTACGGCACTTGCAAGGAGGAGGAGCTGTGACCAAGGAGAA | | | | 1105 |
| Db | 1768 TGTCAAATTGAGTACAGGACTTCAAGGAAGGAGCTGAGAATAGAAGGAGGC | | | | 1827 |
| Qy | 1106 AGAATGAGAAAGATATCAAAAGGAAGATGAGGTGGTC | | | | 1150 |
| Db | 1828 GCAATTGAAATATGTCACAAAGATGACAAAGATGGTTC | | | | 1872 |

Search completed: July 7, 2004, 22:27:51
Job time : 833 secs

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GenCore version 5.1.6
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Run on: July 7, 2004, 16:21:19 ; Search time 5090 Seconds
(without alignments)

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Searched: 27513289 seqs, 14931090276 residues
Perfect score: 1 gaaaatgcgagggttttt.....atgaagaaggttacaattt 1270

Sequence: Total number of hits satisfying chosen parameters: 55026578
Scoring table: IDENTITY_NUC
Minimum DB seq length: 0
Maximum DB seq length: 0
Post-processing: Minimum Match 0%
Listing first 45 summaries

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2: em_estbun: *
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7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
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18: em_gss_inv: *
19: em_gss_p1n: *
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27: em_gss_vrl: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-----------------|---|
| 1 | 693.2 | 54.6 | 741 13 BUG35657 | RESULT 1 LOCUS BUG35657 741 bp mRNA linear EST 23-SEP-2002 DEFINITION 028D02 Infected Arabidopsis leaf Arabidopsis thaliana cDNA, mRNA SEQUENCE sequence. ACCESSION BU635557 VERSION BU635557.1 GI:23302912 KEYWORDS EST. |
| 2 | 673.4 | 53.0 | 694 9 AV784351 | Arabidopsis thaliana (thale cress) ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S. and Wellinder,K.G. |
| 3 | 649.1 | 51.1 | 9 AV823798 | Plants EST sequencing of Erysiphe cichoracearum infected Arabidopsis Unpublished (2002) |
| 4 | 608.4 | 47.9 | 650 14 CB255740 | COMMENT Contact: Karen G. Wellinder Institut for bioteknologi Aalborg Universitet Sohngardsbøllevej 49, 9000 Aalborg, Denmark Tel: +45 9638467 Fax: +45 98141808 Email: kg@bio.auc.dk FEATURES Location/Qualifiers |

| source | Locus | Definition |
|-----------------------|------------|---|
| Query Match | AV784851 | RAFL6 <i>Arabidopsis thaliana</i> cDNA clone RAFL6-08-N18 3', mRNA sequence. |
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| | | /mol_type="mRNA" |
| | | /strain="Columbia" |
| | | /db_xref="taxon:3702" |
| | | /dev_stage="plant 3 weeks old, three days post infection" |
| | | /clone_lib="Infected <i>Arabidopsis</i> Leaf" |
| | | /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of <i>Arabidopsis</i> and <i>E. cichoracearum</i> infected leaf from three weeks old <i>Arabidopsis</i> plants. Plants were harvested 3 days after infection and mRNA oligo dT selected." |
| | | |
| Query Match | 54.6% | Score 693.2; DB 13; Length 741; |
| Best Local Similarity | 98.4% | Pred. No. 1.2e-164; |
| Matches | 732; | Mismatches 0; Indels 4; Gaps 3; |
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| Query | 222 | CGTTGTGATAGTGCACATCTAAGGGTTATGTCCTCTAAAGTGATGACT 281 |
| | 1 | CGTTGTGATAGTGCACATCTAAGGGTTATGTCCTCTAAAGTGATGACT 58 |
| | 282 | GAGGTCTGATGAGAAGTCAGTAAAGCAATTAAAGGAAGTCACGGTCAACCA 341 |
| | 59 | GAGGTCTGATGAGAAGTCAGTAAAGCAATTAAAGGAAGTCACGGTCAACCA 118 |
| | 342 | TCCAGTACTCTACATGCTTGTCACTACAGGCCATGCCAAAAACTCGCACCAA 401 |
| | 119 | TCCAGTACTCTACATGCTTGTCACTACAGGCCATGCCAAAACTCGCACCAA 178 |
| | 402 | TTCAGGATCATGCATGCAACATTATGATGGTTCTGGTAAGCTGGTCACTG 521 |
| | 179 | TTCAGGATCATGCATGCAACATTATGATGGTTCTGGTCAAGAACAGAACCA 238 |
| | 462 | GAACTAGCCGTTAGCCATGGCTTGTGATGAGTCACTCTGGGCGCTTG 521 |
| | 239 | GAACTAGCCGTTAGCCATGGCTTGTGATGAGTCACTCTGGGCGCTTG 298 |
| | 522 | CATGTTGGCTGGGAAANTAGCTTATGGAAAGGAAGAACCTTCTTCCAAATGTTCA 581 |
| | 299 | CATGTGCTGGAAATTAGCTTATGGACKGAGGAACCTTCTTCCAAATGTTCA 358 |
| | 582 | CCTATGGCAACTGTATATGAGTGGAGTTATGGTTGTGAAACAAAGGAGGA 641 |
| | 359 | CCTATGGCAACTGTATATGAGTGGAGTTGTGAAACAAAGGAGGA 418 |
| Db | | |
| Query | 642 | AAGCTCGCAGTGTATGAGTGTAGGAGAAGGATGGTGTGAGACAGAGGA 701 |
| | 642 | AAGCTCGCAGTGTATGAGTGTAGGAGAAGGATGGTGTGAGACAGAGGA 478 |
| | 419 | AAAGCTCGCAGTGTATGAGTGTAGGAGAAGGATGGTGTGAGACAGAGGA 478 |
| | 702 | GATGGAAATTCTCTTTAAGGAGGAAGCTGGAGAACCCATGCCAAAGTAGAATG 761 |
| | 479 | GATGGAAATTCTCTTTAAGGAGGAAGCTGGAGAACCCATGCCAAAGTAGAATG 538 |
| | 762 | GCCATAGCATACATGGGGGAGGATTATGGTGTAGGAGAAGGATGGTGTGAG 703 |
| | 539 | GCCATAGCATACATGGGGGAGGATTATGGTGTAGGAGAAGGATGGTGTGAG 575 |
| | 822 | GCTTGTAGCAATTAAACCCATGCCATCTAACATAGCCTGGCTCATC-AACTAA 880 |
| | 599 | GCTTGTAGCAATTAAACCCATGCCATCTAACATAGCCTGGCTCATC-AACTAA 658 |
| | 881 | ACGATAGATGAGCAATTGGTCACTGCAACATCTGGTGTAGAGAAGAACCC 940 |
| | 659 | ACGATAGATGAGCAATTGGTCACTGCAACATCTGGTGTAGAGAAGAACCC 717 |
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| RESULT 2 | | |
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QY 944 AGCACTGTGAGAAGGAGGAAGCAAGGGAGGTTAGACAGATGACTCAGCACGTC 1003
 Db 334 AGACTGTGAGAAGGAGGAAGCAAGGGAGGTTAGACAGATGACTCAGCACGTC 275
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 QY 1064 AGCACTTGCGACCAAGAGCTTGTACACAAAGCAGGAAGTACAAGAT 1123
 Db 214 AGCACTTGCGACCAAGAGCTTGTACACAAAGCAGGAAGTACAAGAT 155
 QY 1124 ATTCGAAGGAAAGATGAAGGTTGGTGCCTA-GTCAAGAGCCTTTTGGTTGATAGT 1182
 Db 154 ATTCGAAGGAAAGATGAAGGTTGGTGCCTA-GTCAAGAGCCTTTTGGTTGATAGT 95
 QY 1183 TATGGCAATGTTGTTCCCTTTCCTGCTATTTGGACGSCACAGATTAAGC 1242
 Db 94 TATGGCAATGTTGTTCCCTTTCCTGCTATTTGGACGSCACAGATTAAGC 35
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RESULT 3

AV223798 AV823798 669 bp mRNA linear EST 01-APR-2002
 DEFINITION AV823798 RAFL6 Arabidopsis thaliana cDNA clone RAFL6-08-N18 5',
 mRNA sequence.
 ACCESSION AV823798
 VERSION AV823798.1 GI:19865858
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 669)
 AUTHORS Seki,M., Nakasaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
 Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
 Arakawa,T., Shibata,K., Shinagawa,A., Muzumatsu,M., Hayashiaki,Y.,
 and Shinozaki,K.
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9059
 Fax: 81-298-36-9059
 Email: maseki@rc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pliuescript vector as a SstI/XbaI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

Location/Qualifiers

1..669

FEATURES source

/organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"

/clone="RAFL6-08-N18"
 /dev_stage="Plants at various developmental stages from germination to mature seeds"
 /lab_host="DIL10B"
 /clone_lib="RAFL6"
 /note="Site 1: SstI; Site 2: XbaI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatment"

ORIGIN

Query Match

Best Local Similarity 99.1%; Pred. No. 1.8e-153;
 Matches 663; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TCAGAACAAATCTGAAATTATCTCTGGTGTGATCAGTCCTCTGGAGTGC 87
 Db 1 TGGAACTCAAATCTGAAATTATCTCTGGTGTGATCAGTCCTCTGGAGTGC 60
 QY 88 GAGCACGAGGAGTCACTACTCTGAGCTTCATCTCCAGGTGATTGGAA 147
 Db 61 GAGCACGAGGAGTCACTACTCTGAGCTTCATCTCCAGGTGATTGGAA 120

QY 148 ATATGATGTAATCTGAGCTCAACTCAACACATGACAAGGAGGAAATGGT 207
 Db 121 ATATGATGTAATCTGAGCTCAACTCAACACATGACAAGGAGGAAATGGT 180
 QY 208 ACTCGAAGAAGTGGCGTGTGATAGTG-CGCACTCTAACATGACCAAGGAAATGGT 266
 Db 181 ACTGAAGAAGTGGCGTGTGATAGTG-CGCACTCTAACATGACCAAGGAAATGGT 240
 QY 267 GTTGATGATGAGCTGAGCTGAGTGAAGAGTGTGAGATATAAGGAGT 326
 Db 241 GTTGATGATGAGCTGAGTGAAGAGTGTGAGATATAAGGAGT 300
 QY 327 CAGCGTCCAACCATCCAAAGTACTCTACATGCTTGTCACTACAGCGCATGGACAAA 386
 Db 301 CACCGTCCAAACCATCCAAAGTACTCTACATGCTTGTCACTACAGCGCATGGACAAA 360
 QY 387 AACTCGAGCACAATTGAGGATACATGGCATGAGGAGCAACTATGAAATGGTCT 446
 Db 361 AACCTGCGCACAATTGAGGATACATGGCATGAGGAGCAACTATGAAATGGTCT 420
 QY 447 GGAAAGGAAAGAAAGACTAGCGGGTTAGCCATCGTGTGCTACATGAAGTCTG 506
 Db 421 GGAAAGGAAAGAAAGACTACCGGGTTAGCCATCGTGTGCTACATGAAGTCTG 480
 QY 507 GAACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 566
 Db 481 GAACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 567 TTGCCAATGTCACCTATGGCAGCTGTTAGCTGATAGGTTGTTGAT 626
 Db 541 TTTCGATGTTCCACCTATGGCAGCTGTTAGCTGATAGGTTGTTGAT 600
 QY 627 GAAACAGGAGGAAGCTCGAGCTGATAGCTGATAGGAAAGCTGTTGTCGAGCA 686
 Db 601 GAAACAGGAGGAAGCTCGAGCTGATAGCTGATAGGTTGTCGAGCA 660
 QY 687 GACAGAGA 695
 Db 661 GACAGAGA 669

RESULT 4

CB255740 CB255740 650 bp mRNA linear EST 06-NOV-2003
 DEFINITION 23-E012741-027-007-M05-T7R MP1Z-ADTS-027 Arabidopsis thaliana cDNA clone MP1Zp772N057Q 5'-PRIME, mRNA sequence.
 ACCESSION CB255740
 VERSION CB255740.1 GI:3280513
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 650)
 AUTHORS Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
 Mitchell-Ools,T. and Weissenbacher,B.
 TITLE Large-scale identification and analysis of genome-wide
 single-nucleotide polymorphisms for mapping in *Arabidopsis thaliana*
 JOURNAL Genome Res. 13 (6), 1250-1257 (2003)
 MEDLINE 2268290
 PUBMED 12799357

| | |
|-----------------------|--|
| COMMENT | Contact: Weisshaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weisshaar@mpiz-koeln.mpg.de Insert Length: 650 Std Error: 0.00 Plate: 7 row: M column: 05 Seq primer: T7R: CTAATACGACTCACTATAGGGA. |
| FEATURES source | <p>Location/Qualifiers</p> <p>1. .650</p> <p>/organism="Arabidopsis thaliana" (mol_type="mRNA") (cultivar="Eifel-2 (E1-2)") (db_xref="GABI:522595" (clone="MPIZp772m0570"</p> <p>/tissue type="whole plant" (dev_stage="adult plant, mixed stresses" (lab_host="E. coli TOP10" (clone lib="MPIZ-ADIS-027"</p> <p>/note="vector: pSPPRT; Site:1: Sali; Site:2: NotI; cDNA library from Arabidopsis thaliana, accession Eifel-2; ten week old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2) at 37 Grad-C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a foreeces, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 M-0C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sali-NotI, primer sites and orientation:</p> <p>T7-SalI-CCACCGCGCG-5prime-cDNA-PolyA-CC-NotI-SP6; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection'. PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."</p> |
| ORIGIN | |
| Query Match | 47.9% Score 608.4; DB 14; length 650; |
| Best Local Similarity | 98.1%; Pred. No. 3.5e-143; |
| Matches | 628; Conservative 0; Mismatches 11; Indels 1; Gaps 1; |
| QY | ATTATCTCTGGTGTATCGTCAGTCGAGTGACTCCAGCACGAGCTCAC 105 |
| Db | 13 ATTATCTCTGGTGTATCGTCAGTCGAGTGACTCCAGCACGAGCTCAC 72 |
| QY | 106 TACTCTGAGCTCTCATCTTACCCAGGTGATTGGAAATAATGGATGATCTG 165 |
| Db | 73 TACTCTGAGCTCTCATCTTACCCAGGTGATTGGAAATAATGGATGATCTG 132 |
| QY | 166 GAGCTCAACACTCAAACATGCAAGAGGAAATGTTACTGAGGAGCTGCCT 225 |
| Db | 133 GAGCTCAACACTCAAACATGCAAGAGGAAATGTTACTGAGGAGCTGCCT 192 |
| QY | 226 GTCTGAGATG-GCCATCTCAAGAGGTAATGTTCTCTTAAGTGTAGGAGCTG 284 |
| Db | 193 GTGCATAGTAGCTGCACTCTCAAGAGGGTAATGTTCTCTTAAGTGTAGGAGCTG 252 |
| QY | 285 GTCTGAGATGAGAAGTCACTAAGGAGATAATAAGGAAGTCAAGGTCCAAACATCC 344 |
| Db | 253 GTCTGGAGAGAAGTCACTAAGGAGATAATAAGGAAGTCAAGGTCCAAACATCC 312 |
| QY | 345 AAGTACTCTCATGCTTGTCACTACAGGCAATGAGCAAAACTCCAGACAATT 404 |
| Db | 313 AAGTACTCTCATGCTTGTCACTACAGGCAATGAGCAAAACTCCAGACAATT 372 |
| RESULT 5 | |
| DEFINITION | CAB7003_IvAr_F02 cabernet Sauvignon Berry Post-Veraison - CAB7 |
| LOCUS | CB981020 |
| ACCESSION | Vitis vinifera cDNA clone CAB7003_IvAr_F02 3', mRNA sequence. |
| VERSION | CB981020.1 |
| KEYWORDS | EST. |
| REFERENCE | |
| AUTHORS | Vitis vinifera |
| ORGANISM | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis. |
| TITLE | Expressed sequence tags from cabernet sauvignon berries at various developmental stages |
| JOURNAL | Unpublished (2003) |
| COMMENT | Contact: Douglas Cook, PhD UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: dcoo@ucdavis.edu Seq primer: GCCTAACGATGCTCTAG. |
| FEATURES source | <p>Location/Qualifiers</p> <p>1. .892</p> <p>/organism="Vitis vinifera" (mol_type="mRNA") (cultivar="Cabernet Sauvignon" (db_xref="Taxon:29760" (clone="CAB7003_IvAr_F02" sex="Hermaphrodite" (dev_stage="Post-Veraison, 18-19 brix" (lab_host="DH5alpha" (clone lib="Cabernet Sauvignon Berry Vector: DPNR; Site:1: SfII; Site:2: SfiI; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8 berries. Samples were collected post-veraison from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental vineyard. cDNAs were made by oligo-dT priming and directly cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGTATACGAGAGGAGGCCATACGCCCG-3', and 5'-ATTCATAGGCCAGGGGCCACANG-dT(30)NN-3'. Library was constructed using the ClonTech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."</p> |
| ORIGIN | |

| | | |
|-----------------------|--|---|
| Query Match | 38.6% | Score 490; DB 14; Length 892; |
| Best Local Similarity | 77.0% | Pred. No. 3.7e-113; Mismatches 181; Indels 1; Gaps 1; |
| Matches | 609; | Conservative 0; Mismatches 181; Indels 1; Gaps 1; |
| Accession | AY105475 | CTGGAGCATCAAACACTGATCAGGAGATGAATAGTACTGAGGAATGCC 222 |
| Version | AY105475.1 | CTGCAAGTAAACACTGATCAGGAGATGAATAGTACTGAGGAATGCC 222 |
| Source | Zea mays | CTGCAAGTAAACACTGATCAGGAGATGAATAGTACTGAGGAATGCC 222 |
| Organism | Zea mays | CTGCAAGTAAACACTGATCAGGAGATGAATAGTACTGAGGAATGCC 222 |
| RESULT 6 | | |
| LOCUS | AY105475 | AY105475 mRNA sequence. |
| DEFINITION | Zea mays | PC0126522 mRNA sequence. |
| ACCESSION | AY105475 | PC0126522 mRNA sequence. |
| VERSION | AY105475.1 | GI:21208553 |
| KEYWORDS | HTC | |
| SOURCE | Zea mays | |
| ORGANISM | Bakteria; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae; Tracheophyta; Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; PACAD | |
| REFERENCE | 1 | (bases 1 to 1363) |
| AUTHORS | Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanefey,M., Moreante,M. and Tingey,S.V. | |
| TITLE | Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes | |
| JOURNAL | Unpublished (2002) | |
| COMMENT | 2 (bases 1 to 1363) | |
| REFERENCE | Coe,E.H. | |
| AUTHORS | Direct Submission | |
| TITLE | JOURNAL | |
| Db | 160 | TTTGTGATGGGAACTCTCTCAAGATGGTAACTGAGTAAATGAGTAAATGAGCA 160 |
| Qy | 161 | TTTGTGATGGGAACTCTCTCAAGATGGTAACTGAGTAAATGAGTAAATGAGCA 160 |
| Db | 160 | TTTGTGATGGGAACTCTCTCAAGATGGTAACTGAGTAAATGAGTAAATGAGCA 160 |
| Qy | 160 | TTTGTGATGGGAACTCTCTCAAGATGGTAACTGAGTAAATGAGTAAATGAGCA 160 |
| Db | 220 | GAGGTCTGGTGGAGAGTCAGTAAGCAGGATTAAAGGAGTCACGGTCCAAACCA 341 |
| Qy | 220 | GAGGTCTGGTGGAGAGTCAGTAAGCAGGATTAAAGGAGTCACGGTCCAAACCA 341 |
| Db | 280 | GAACTCTCTCATGAGAACGACAAAGGAGTCAGTGAAGGAGTCATGGTCAAACCA 280 |
| Qy | 280 | GAACTCTCTCATGAGAACGACAAAGGAGTCAGTGAAGGAGTCATGGTCAAACCA 280 |
| Db | 340 | TTCAGTACTCTACATGTTCTGGATTAGGGCATGACTGAAAGCACCGACAG 340 |
| Qy | 340 | TTCAGTACTCTACATGTTCTGGATTAGGGCATGACTGAAAGCACCGACAG 340 |
| Db | 400 | TTTGAGGATCATGGATGGGACCAATTATGATGGTCITGGAAAGGAAAGAAA 400 |
| Qy | 400 | TTTGAGGATCATGGATGGGACCAATTATGATGGTCITGGAAAGGAAAGAAA 400 |
| Db | 460 | GAACTAGCCGTTAGCCATGGGTTGCTAGCATGAAGCTCTGGTAACGGCTTG 521 |
| Qy | 460 | GAACTAGCCGTTAGCCATGGGTTGCTAGCATGAAGCTCTGGTAACGGCTTG 521 |
| Db | 520 | CATGTTGGTGGGATTAGCTTATGGAAAGAAGGAAACTTCTTCCCATACTG 581 |
| Qy | 520 | CATGTTGGTGGGATTAGCTTATGGAAAGAAGGAAACTTCTTCCCATACTG 581 |
| Db | 580 | CCTATGGCAGACTGTATAGTGGTGGAGTTATGGTGTGAAACAAAGGAGGA 641 |
| Qy | 580 | CCTATGGCAGACTGTATAGTGGTGGAGTTATGGTGTGAAACAAAGGAGGA 641 |
| Db | 640 | AAAGCTCGGAGTATGGTGTGAAAGGAGATGGTCAGGAGACAGGAAATG 701 |
| Qy | 640 | AAAGCTCGGAGTATGGTGTGAAAGGAGATGGTCAGGAGACAGGAAAGGT 640 |
| Db | 701 | GATGGAATGTTACTCTCAGGGAAACACTAGGGAGCTATGGAGGTATGAAATG 700 |
| Qy | 701 | GATGGAATGTTACTCTCAGGGAAACACTAGGGAGCTATGGAGGTATGAAATG 700 |
| Db | 761 | GCCATAGCATACATGGGAGCTGGTTTACGGCTATGGTCAACTAA 821 |
| Qy | 761 | GCCATAGCATACATGGGAGCTGGTTTACGGCTATGGTCAACTAA 821 |
| Db | 760 | GCCATAGCATACATGGGAGCTGGTTTACGGCTATGGTCAACTAA 821 |
| Qy | 760 | GCCATAGCATACATGGGAGCTGGTTTACGGCTATGGTCAACTAA 821 |
| Db | 820 | GCTTCTAGGTTAAACCCATGCATCTAACATAGCAGCTGCTCCTCATCAAATAAA 881 |
| Qy | 820 | GCTTCTAGGTTAAACCCATGCATCTAACATAGCAGCTGCTCCTCATCAAATAAA 881 |
| Db | 820 | GCTTCTAGGTTAAACCCATGCATCTAACATAGCAGCTGCTCCTCATCAAATAAA 881 |
| Qy | 820 | GCTTCTAGGTTAAACCCATGCATCTAACATAGCAGCTGCTCCTCATCAAATAAA 881 |
| Db | 880 | CGATACGATGAGGAGCTGCTACTGCAACATGCTGAGGAGAAACCA 941 |
| Qy | 880 | CGATACGATGAGGAGCTGCTACTGCAACATGCTGAGGAGAAACCA 941 |
| Db | 880 | CGATACGATGAGGAGCTGCTACTGCAACATGCTGAGGAGAAACCA 941 |
| Qy | 880 | CGATACGATGAGGAGCTGCTACTGCAACATGCTGAGGAGAAACCA 941 |
| Db | 952 | AAAGCAGCTGT 952 |
| Qy | 952 | AAAGCAGCTGT 952 |
| Db | 891 | AAGCATATT 891 |
| Qy | 891 | AAGCATATT 891 |
| ORIGIN | | |
| Query Match | 36.6% | Score 464.4; DB 11; Length 1363; |
| Best Local Similarity | 71.6% | Pred. No. 1 2e-106; Mismatches 251; Indels 2; Gaps 2; |
| Matches | 637; | Conservative 0; Mismatches 251; Indels 2; Gaps 2; |
| Accession | QY | 237 CCATCTGAGGGCTATGTTCTCCAACTGATGTTGAGCTGGGCTCTGGATG 296 |
| Version | Db | 222 CTCRCCCGGATGGCAGCGCCGCCGGTCTCTGACATGGGCCCTACGAC 281 |
| Source | Qy | 297 AAAGTCAGAAGGATATAAGGAGGTACGGTCCAAACCATCCAGTACTCTACA 356 |
| Organism | Db | 282 AAGGTTAAGGAGCAATCATCAAGAAGGCCATGGCAGGAACCGCTGAGTCGGACG 341 |
| Db | 341 | TGCTTCTGCTACTACAGGGCTGACCTGGTCAAGGATCATGGATAATTGAGGATACCTGG 416 |
| Qy | 341 | TGCTTCTGCTACTACAGGGCTGACCTGGTCAAGGATCATGGATAATTGAGGATACCTGG 416 |
| Db | 416 | 342 TGCTTCTGCTACTACAGGGCTGACCTGGTCAAGGATCATGGATAATTGAGGATACCTGG 401 |
| Qy | 416 | 342 TGCTTCTGCTACTACAGGGCTGACCTGGTCAAGGATCATGGATAATTGAGGATACCTGG 401 |
| Db | 476 | 417 CATGAGGAGCACTTATGAACTGGTCTGGAAAGGAAAGACTACGGGTTA 476 |
| Qy | 476 | 417 CATGAGGAGCACTTATGAACTGGTCTGGAAAGGAAAGACTACGGGTTA 476 |
| Db | 476 | 402 CAAGGAGCACTCAATGAACTGAGGATGAAAGGAAACCA 461 |
| Qy | 476 | 402 CAAGGAGCACTCAATGAACTGAGGATGAAAGGAAACCA 461 |
| Db | 521 | 477 GCCATCGGTTCTACATGGCTCTGGTCAAGGAGCTGGCTGGTCAAGGAGCTGGAA 536 |
| Qy | 521 | 477 GCCATCGGTTCTACATGGCTCTGGTCAAGGAGCTGGCTGGTCAAGGAGCTGGAA 536 |
| Db | 596 | 462 GGCTCGGTTGCGACATGAAAGGGAGCGCTGATGTTGCTGGTGGAG 521 |
| Qy | 596 | 462 GGCTCGGTTGCGACATGAAAGGGAGCGCTGATGTTGCTGGTGGAG 521 |
| Db | 581 | 537 TTAGCTTATGAAAGGAGAACTTCTTCCATGTTCTACATGGCTGGAGCTGG 596 |
| Qy | 581 | 537 TTAGCTTATGAAAGGAGAACTTCTTCCATGTTCTACATGGCTGGAGCTGG 596 |
| Db | 581 | 522 CTAGGCTTGGCAAGGAGTTTCATCCAAATGTCCTCCAAATGCCAGACCT 581 |
| Qy | 581 | 522 CTAGGCTTGGCAAGGAGTTTCATCCAAATGTCCTCCAAATGCCAGACCT 581 |
| Db | 656 | 597 TTTATGAGGAGGTTGAGGTTGAGAACAGGAGAACAGCTGGAGCTG 656 |
| Qy | 656 | 597 TTTATGAGGAGGTTGAGGTTGAGAACAGGAGAACAGCTGGAGCTG 656 |
| Db | 641 | 582 GTTATGAGGAGCTCATGGTATGTTGAGCTGGTCAAGGAGCTGG 641 |
| Qy | 641 | 657 ATGACTCTAGGAGAACGATGGTGCAGCAGAGAAATGGTGGGATTCTCT 716 |
| Db | 716 | 642 ATGACGTTGAGGAGGATGGCTGAGCAGGAGAACAGTGGAGCTGGAT 701 |
| Qy | 701 | 717 TTAGGAGGAGAACTGGAGAACGATGGCAGAGAACAGTGGAGCTGGAT 776 |

Query Match 35.4%; Score 449.6; DB 14; Length 972;
 Best Local Similarity 70.0%; Pred. No. 6.5e-03; Index 1;
 Matches 619; Conservative 0; Mismatches 264; Gaps 1;

Db 702 TTCAGAAGAAAGAAGCTTGGGAGGCCATGCCAGGAATGTGAATGGCGATGTCATACTG 761
 Qy 777 GGAGCAGATTGTGTTTCACTGCCTATGGCTTACCCAGATACTGCTTAGAGTTAA 836
 Db 762 GGAGATGATTTCATGTTCTCATTAATTGGAAGTAGAGAACATAGGCATGGCCCTGGCCTGGAA 821
 Qy 837 AACCATGCCCCTAACCTAACAGCTGCTGCTCAACTAAACGATAGCATGGAA 896
 Db 822 AATCCATGCCCCTAACAGCTGCTGCTGATGCTGATCAAACCTAAAGAGATTCGATGAACT 881
 Qy 897 ATGGCTACTGCAACATGTGTTGACAGAGAAAGAAAACCCAAAAGCACTGTTGAGA 956
 Db 882 ATGGCCAGTGTAGATGTTGACAGAGATGAGATGTCAMQGCCTGTTGAG 941
 Qy 957 AGAGGAAAGCAAGGCAAGGCAAGGCTGCTGAGCTGACTCGAGCTGATGTTCCGAAG 1016
 Db 942 CGAGGAAACATTAATCTGACTTGCCAGACACA-AAGCGAGGAAAGATTCCTCAA 1000
 Qy 1017 GCACAAAGTAGTCCTGAGCACAGGCAATAGAGAGACTGAGGACACTGAGAG 1076
 Db 1001 GCGAGAACTGACTCCAGAGACAGGAGATCTCGGAGCTCGCTGCTCGCGAA 1060
 Qy 1077 CAAGAGAACCTTGTACCAAAAGCAGAAAGAATGACAAAGGAAATT 1126
 Db 1061 CAAAGACAGGCACT-TACCGAAGCAGAGGAGCTCTACAAAGGCTCT 1109
 Qy 300 GTCACTTACAGGAGTATTAAGGAGGTCACSGTTCACAACTCCAGTACTCTAGTC 359
 Db 200 GTCATAAAGCAATTATCAAGAGSCATGGACAAAGCCATCAACATCAGCAACTG 259
 Qy 360 TTTGTGACTACAGGGATGGACAAACACTGCAGGACAAATTGGGATACATGCAT 419
 Db 260 TTCTTACATACAGGAGATGGTCAGAGAACTTGAGAATTTGAGATACTGCTA 319
 Qy 420 GAGCAGACACCTATGATGATGTTCTGAAAGAGAAAAGAGAACTAGCCGTTAGCC 479
 Db 320 GAACACACACCTTGTGACTGTTGAGTTGAGAALAGAAAGAAGAATGTCGGCCTTGCC 379
 Qy 480 ATCGTGTGCTAGCATGAGCTGGCAACTCGCGATGTCATGTTGGGATTA 539
 Db 380 ATTGGAGATGCAAGCATGAGCTGAGAATGTCGGAGCTGGTGAATGTTGGATTA 439
 Qy 540 GCTTATGGAAGAGGAAACTTCTTCCATGTTCCACCTTGGCACTGTTGGAACTGTTA 599
 Db 440 GGATATGGGAGAAGGAAATTCTCTTCCAAUTGCGCCCGTGTGAGATTTGA 499
 Qy 600 TAGGAGGGAAGTATATGGGTTGAGAACAAAGGGAAAGCTCGCAGTGTGATG 659
 Db 500 TATGAGTGTGAGCTGATGTTGAGATATCAAGAGGAGGTAGAGTGCATG 559
 SOURCE
 ORGANISM Allium cepa (onion)
 Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Alium; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Aliaceae;
 REFERENCE 1 (bases 1 to 972)
 AUTHORS Harvey, M.J.; Cheung, F.; Van Aken, S.; Utterback, T. and Town, C.D.
 TITLE Expressed Sequence Tags from a normalized library of mixed onion
 tissues (Allium cepa)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Harvey MJ
 Department of Horticulture
 USDA-ARS and University of Wisconsin
 1575 Linden Drive, Madison, WI 53706, USA
 Tel: 608-263-1830
 Fax: 608-263-4743
 Email: mjhavrey@facstaff.wisc.edu
 TIGR sequence name ACID013R. For more information:
<http://havreylab.hort.wisc.edu>
 Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES source
 Location/Qualifiers
 1. -972
 /organism="Allium cepa"
 /note="mRNA"
 /cultivar="Red Creole(bulbs)", unknown(callus), Ebano &
 Texas Legend(roots)"
 /db_xref="ACACD15"
 /clone="ACACD15"
 /tissue type="Callus, roots, and young bulbs"
 /clone Lib=normalized cDNA library of onion"
 /note="vector: pCMVSPORT6-1-ccdb (Invitrogen); Site 1:
 EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA
 from callus, roots, and young bulbs were combined to
 synthesize the library. Normalization to enrich for
 low-copy transcript was performed by proprietary
 techniques of Invitrogen."

RESULT 7
 CF436078
 DEFINITION EST672423 normalized cDNA library of onion Allium cepa cDNA clone
 ACCESSION CF436078
 VERSION 1
 KEYWORDS EST
 SOURCE
 ORGANISM Allium cepa
 Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Alium; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Aliaceae;
 REFERENCE 1 (bases 1 to 972)
 AUTHORS Harvey, M.J.; Cheung, F.; Van Aken, S.; Utterback, T. and Town, C.D.
 TITLE Expressed Sequence Tags from a normalized library of mixed onion
 tissues (Allium cepa)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Harvey MJ
 Department of Horticulture
 USDA-ARS and University of Wisconsin
 1575 Linden Drive, Madison, WI 53706, USA
 Tel: 608-263-1830
 Fax: 608-263-4743
 Email: mjhavrey@facstaff.wisc.edu
 TIGR sequence name ACID013R. For more information:
<http://havreylab.hort.wisc.edu>
 Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES source
 Location/Qualifiers
 1. -972
 /organism="Allium cepa"
 /note="mRNA"
 /cultivar="Red Creole(bulbs)", unknown(callus), Ebano &
 Texas Legend(roots)"
 /db_xref="ACACD15"
 /clone="ACACD15"
 /tissue type="Callus, roots, and young bulbs"
 /clone Lib=normalized cDNA library of onion"
 /note="vector: pCMVSPORT6-1-ccdb (Invitrogen); Site 1:
 EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA
 from callus, roots, and young bulbs were combined to
 synthesize the library. Normalization to enrich for
 low-copy transcript was performed by proprietary
 techniques of Invitrogen."

RESULT 8
 CF417393
 DEFINITION CF417393
 Locus USDA-PP115000-323 Citrus sinensis
 leaves/stems from field collected Valencia orange Citrus sinensis
 cDNA clone IDFL-004_G02 5', mRNA sequence.
 ACCESSION CF417393
 VERSION CF417393.1
 GI:34418520

| | |
|------------|---|
| KEYWORDS | EST. |
| SOURCE | Citrus sinensis |
| ORGANISM | Citrus sinensis |
| REFERENCE | Shatters, R.G., Jr., Chaparro, J.X., Bausher, M.G., Hunter, W.G. and Nedz, R.P. |
| TITLE | Expressed Sequence Tags from Insect-Damaged Field-Collected Sweet Orange (Citrus Sinensis (L.) Osbeck) Immature Leaves and Stems |
| JOURNAL | Subtropical Insects Research Unit, USDA, U.S. Horticultural Research Laboratory, 2001, South Rock Road, Port Pierce, FL 34945, USA |
| COMMENT | Contact: Shatters, Jr. RG Fax: 772 462 5912 Email: rshatters@ushrl.ars.usda.gov |
| FEATURES | Seq primer; T3 Primer; Location/Qualifiers |
| source | 1..710 <mol type="mRNA"/> <organism="Citrus sinensis"/> <mol type="mRNA"/> <isolate="mixed field population"/> <cultivar="Valencia"/> <db_xref="txon:2711"/> <clone="IDFL-004_G02"/> |
| | /tissue type="Flush leaves and stems" /clone lib="Citrus sinensis: Insect-damaged immature leaves/stems from field collected Valencia orange" <note><vector: pBluescript SK(-); site_1: EcoRI; site_2: XbaI; Citrus sinensis (L.) Osbeck; Standard library construction protocols from Stratagene cDNA synthesis kit (Cat.# 200401-5) and Uni-ZAP XR vector kit (cat.# 237211)</vector> were followed using poly(A) RNA." |
| ORIGIN | Query Match 33.8%; Score 429; DB 14; Length 710; Best Local Similarity 76.5%; Pred. No. 1e-97; Indels 1; Gaps 1; Matches 539; Conservative 0; Mismatches 165; Delins 1; |
| QY | 903 CACTGCAACATTGTGTACAGAGAGAACCAAAGCACTTCAAGAGGG 962 |
| Db | 481 CAATGCAGCCTGTTATCGGAGGATTAATGTGAAAGCCCTTTCAAGAGGA 540 |
| QY | 963 AAGCAAGGCGAGCTAGGACGATGACTAGCAGATGATGATGATGATG 1022 |
| Db | 541 AACGCTAGGACAGACTTGGCAACAGATGCTGCCGGAGACTTCTAAAGGAGT 600 |
| QY | 1023 AAGTAGTCCTGAGCAAGGGATTAGAAGAGAGTACAGCACTTGAGAGAGA 1081 |
| Db | 601 AAATTGCACTGAGGAAATGACGGGACCTTGCTGAGCAACTTGTGCAACTG 660 |
| QY | 1082 GAAGCTTGTACCAAGCAGAAATGTCACAAGGAATT 1126 |
| Db | 661 AAAGCTGTATAAAGAGCAAAAGGAGATCTATAAGGAAATT 705 |
| RESULT | 9 |
| CAT65208 | CA765208 839 bp mRNA linear EST 08-JAN-2003 |
| DEFINITION | AF53-RP_06_K05_R7-029.ab1 IRII Drought Stress Panicle Library |
| ORGANISM | Oryza sativa (indica cultivar-group) |
| ACCESSION | CA765208 |
| VERSION | 2 |
| KEYWORDS | cis-trans isomerase (Cyclophilin) (PPIase), mRNA sequence. |
| EST. | CA765208.2 GI:27546946 |
| SOURCE | Oryza sativa (indica cultivar-group) |
| ORGANISM | Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartidae; Oryzeae; Oryza. |
| REFERENCE | 1 (bases 1 to 839) |
| AUTHORS | Bennett,J., Arumugam,K., Lafitte,R., Wen,J., Rudd,S. and Bruskiewich,R.M. |
| TITLE | IRRI Drought Stress Panicle cDNA Library |
| JOURNAL | Unpublished (2002) |
| COMMENT | On Dec 2, 2002 this sequence version replaced gi:25994463. |
| | Contact: Richard Bruskiewich Biometrics and Bioinformatics Unit International Rice Research Institute DAPD 7777, Metro Manila, Philippines Tel: +63 2-845-0563 Fax: +63 2-845-0565 Email: r.bruskiewich@cgiar.org International Rice Information System (IRIS): http://www.iris.irri.org/ ; D0202164 Assignment of putative function to the sequence by S. Rudd of the Munich Information Center for Protein Sequences (http://mips.gsf.de) plate: 06 row: K column: 05. |
| FEATURES | Location/Qualifiers |
| source | 1..839 <mol type="mRNA"/> <organism="Oryza sativa (indica cultivar-group)"> <mol type="mRNA"/> <cultivar="IR64"/> <db_xref="txon:39946"/> <clone="CO002165"/> |
| | /tissue type="panicles" <dev_stage="flowering"> <clone lib="IRRI Drought Stress Panicle Library"> <note><vector: pBluescript II SK+; Water stress was applied by not watering for 4 consecutive days. Panicles were collected from control (well watered) and stressed plants at 2 days before heading, at heading, 50% flowered and 4 days after 50% flowering.</vector> |
| ORIGIN | Query Match 31.1%; Score 395.6; DB 14; Length 839; Best Local Similarity 74.4%; Pred. No. 3.1e-99; Indels 1; Gaps 1; Matches 51; Conservative 0; Mismatches 175; Delins 1; |
| Db | 723 GAGGAGAACTGGAGGAGCATCACAGTATGCAATGGCATCATGGGAC 782 |
| QY | 663 GTAGAGGAAGGATGGTGGCAGCAGAGAAAATGGATGGAAATTCCTTTAG 360 |
| Db | 241 GTCGAGAGAAGGATGGCAGCAGAGAAAATGGATGGAAATTCCTTTAG 300 |
| QY | 783 GATTTATGTTCACTGGCTGGAGGACAGTATGGCTAGCTTAAACCA 842 |
| Db | 361 GACTGATGTTCCAGTTGGAGTACCGGATATGGTTGGCTTAAGATCCA 420 |
| QY | 843 TGCCATCTAACATAGCAGCTGCATCAACTAAAGATACTAGTGAAGAATGGT 902 |
| Db | 421 TGCCATCTAACACGGCAGCATGCTTAAAGCTCAAGTGTAGGAAAGCCATCGG 480 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|--|------|---|-----|---|-----|----|-----|--|-----|----|----|---|-----|----|-----|--|-----|----|-----|---|-----|----|-----|--|-----|----|-----|---|-----|----|-----|---|-----|----|-----|---|-----|----|-----|--|-----|----|-----|---|-----|----|-----|--|-----|----|-----|--|-----|----|-----|--|-----|----|-----|--|-----|----|-----|---|-----|----|-----|--|------|----|-----|---|-----|----|-----|--|------|----|-----|---|-----|
| QY | 441 | GTCCTTGAAAGAGAAAGAACTAGCGGTTAGCCATCGGGTCTAGGTGANG | 500 | Tel: 612 624 2755 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 21 | GTAATGGAAAGAGAAAGAAACAGTCTGGTTAGCATGCTGGTTGCTAAGCA | 80 | Fax: 612 625 1738 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 501 | TCTGGTGAAGCTGGCTGTGCAGTGTGGGAATTAGCTATGGAAAAGAGAAC | 560 | Email: kvandenbosch.umn.edu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 81 | AGTGGGAGAGATGCACTGTGGCTGGTGGGGAGTAGCTATGGAAAAGAGAAC | 140 | Texas A&M EST name: T257055e | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 561 | TTTCCTTCCCAATGTCCTCAAATGGCAGCTTATATGAGGTGGATTGG | 620 | TIGR sequence name: MTEAM60TK | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 141 | TTTCATCCCAATGTCCTCAAATGGCAGCTTATATGAGGTGGATTGG | 200 | More information is available at: http://chrysalie.tamu.edu/medicago | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 621 | TTTGATGAAACAAGAGAAAGACTCGAAGTGTAGTGTAGGAGAAAGATGG | 680 | Seq primer: Skmod (CTA gAA CTA gtg gAT CC) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 201 | TTTGATGATCTCAAGAGGGAAAGCCGAGTGAAGTGA | 260 | /db_xref="Skmod" /location /Qualifiers | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 681 | GCAGCGACAGAGAAATGGATGGAACTCTCTTAAAGGAGAGAACTGGAGGA | 740 | 1..650 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 261 | GCAGCGACAGAGAAATGGATGGAACTCTCTTAAAGGAGAGAACTGGAGGA | 740 | /organism="Medicago truncatula" | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 621 | TTTGATGAAACAAGAGAAAGACTCGAAGTGTAGTGTAGGAGAAAGATGG | 680 | /mol_type="mRNA" | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 201 | TTTGATGATCTCAAGAGGGAAAGCCGAGTGAAGTGA | 260 | /cultivar="genotype A17" | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 741 | GCCATCCAACTGATGAAAGGGAAAGCCGAGTGTGCAATACAGGAGATTC | 800 | /db_xref="Taxon:3880" | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| QY | 801 | TATGGAAAGTACAGGATGAGATAGCTTGAGGAGATTCAGGAGAACTGGAGGA | 380 | /tissue_type="seedling roots" | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 381 | TTGGGAAATAACAGAGATAGCTTGAGGAGATTCAGGAGAACTGGAGGA | 380 | /dev_stage="3 days post-inoculation with Sinorhizobium meliloti" | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 861 | GCTGCTCATCAACTAAACGATAGATGAGCAATGGTCACTGCCACA-TTGTGT | 919 | /lab_host="E. coli strain XLOR" | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| QY | 920 | GACAGAGAGAGAAACCCAAAGACACTGTTAGCAAGAGGGAAAGCAGGGAGCT | 979 | /vector: pBlueScript SK -; Site_1: EcoRI; Site_2: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 501 | GGCAGAGGATGAAACAACTGATGAAAGCATTCCTGAGCAGGAAAGCAGAGCT | 560 | xhol: cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the UniZap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOR cells." | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 980 | AGGACAGATGACTCGCACTGAGATTCGGAAAGGCCAAAGTAGTGTCTGCA | 1039 | QY | 403 | TTGAGGATACATGCGATGAGCTGGGGTCTGAGTGTAGTGTCTGCA | 462 | QY | 463 | AACCTAGGGTTAGCCATCGGGTCTGAGTGTAGTGTCTGCA | 522 | QY | 62 | AATGAGATACATGCGATGAGCTGGGGTCTGAGTGTAGTGTCTGCA | 121 | QY | 523 | ATGTGCTGGGATTAGCTTATGGAAAGGAAAGCTTCTTCTCCAAATGTCAC | 582 | Db | 621 | CAAGGAGATCAGCGTGGCTCTCGGGAAACAGGATAAAGCTGTACCAA | 680 | Db | 122 | GTGTAAGCTGGAAATTAGATGAGTGGAGTATTGAGGAACTTTCATGTCAC | 181 | QY | 583 | CTATGGCAGACTTGTATAGATGAGTGGAGTATTGAGGAACTTTCATGTCAC | 642 | Db | 182 | CAATGGCAGATTAGTGTAGTGTAGGAGTCATGTTGATGAAACAGGAGGA | 241 | QY | 643 | AAGCTCGGTGATATCTGTAGAGAAAGATGCTGAGCAGAGAAATGG | 702 | Db | 242 | AAGCTCGGTGATATCTGTAGTGTAGGAGAAAGCTGGGGAGGGATGGAGAAGTGG | 301 | QY | 703 | ATGGGATTCCTTCTTCTGGAGGAGAACTGGGGAGCCATGCAACAGTGTAGTGG | 762 | Db | 302 | ATGGGATTCCTTCTGGAGGAGAACTGGGGAGCCATGCAACAGTGTAGTGG | 361 | QY | 763 | CCATAGCATACAGGGGAGCAAGTGTGTTAGCTGAGTGTGGAGATGG | 822 | Db | 362 | CCATAGCATACAGGGGAGCAAGTGTGTTAGCTGAGTGTGGAGATGG | 421 | QY | 823 | CITTAGCGAGTAAACCCATCCATTAACATASAGCTGCTCTCAACTAAC | 882 | Db | 422 | CTCTGGCTGAAAGAATCATGCGATCTTAACAGCGGGCGCTGCTGATGAC | 481 | QY | 883 | GATAGCTGAGGATGGCTGAGTGTGGAGTGTGGAGATGG | 1002 | Db | 482 | GCTATGGAGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG | 541 | QY | 943 | AACACTCTGAGAGGGAAAGCAAGGGAGCTAGGAGAGCTAGGAGCTG | 1002 | Db | 542 | AGGTTTATAGGAGGTGAGCTAGGAGCACTGGGGAGAGCACTGGTGTGNGCAGG | 601 |

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 DEFINITION EST3222 Kv3 Medicago truncatula cDNA clone pkv3-15123, mRNA
 ACCESSION AW773636
 VERSION 1
 KEYWORDS EST,
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 1 (bases 1 to 650)
 Vandenbosch, K., Hurt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,
 Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
 Fraser, C.M.
 ESTs from roots of Medicago truncatula after Rhizobium inoculation
 Unpublished (1999)
 Contact: Vandenbosch, K
 Department of Plant Biology
 University of Minnesota
 220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA

REFERENCE

JOURNAL

COMMENT

| | | | |
|-----------------|---|---|---|
| QY | 1003 ATGATTCGCAAGGCCAAGCATGCCCTGAGATAAGCAATT 1049 | Db | 367 ATTGACTAGTGAATGGAAAAGAAAAACAAATGTCTGGTTAGGCATTGGTTGCT 426 |
| Db | 602 AAGATTCCTAANAGGCCAAGCATGCCCTGAGATAAGCAATT 648 | QY | 492 AGCTGAAAGTCTGCTGAAACGTCGCTGTGCACTGTGGTGGAAATTACCTATGGAA 551 |
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| QY | Oryza sativa (japonica cultivar-group) | ORGANISM Oryza sativa | KEYWORDS |
| QY | 1 (bases 1 to 812) | REFERENCE Jantsurivarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. | AUTHORS |
| QY | Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea | JOURNAL Unpublished (2003) | TITLE |
| QY | Contact: Rod Wing | COMMENT | |
| QY | Arizona Genomics Institute | University of Arizona | |
| QY | Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA | Address | |
| QY | Tel: 520 626 3988 | Fax: 520 621 9388 | |
| QY | Email: http://genome.arizona.edu | PCR Primers | |
| QY | FORWARD: gta aaa cga cgg tat cca gtg | FORWARD: | |
| QY | BACKWARD: gga aac agc tat gag cat g | BACKWARD: | |
| QY | Plate: 16 row: L column: 13 | Plate: | |
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| QY | Query Match Score 29.9%; Best Local Similarity 73.0%; Pred. No. 2.4e-85; Matches 501; Conservative 0; Mismatches 184; Indels 1; Gaps 1; | Match | |
| QY | 193 GAGAGGAAATAGTTACTAGAGGAGTCCCGTGCTGATAGTGGCCATCTCAAGGGT 251 | Match | |
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| QY | Oryza sativa (japonica cultivar-group) | ORGANISM Oryza sativa | KEYWORDS |
| QY | EST. EST 09-APR-2003 | REFERENCE | |
| QY | 1 (bases 1 to 812) | AUTHORS | |
| QY | Jantsurivarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. | JOURNAL Unpublished (2003) | TITLE |
| QY | Contact: Rod Wing | COMMENT | |
| QY | Arizona Genomics Institute | University of Arizona | |
| QY | Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA | Address | |
| QY | Tel: 520 626 3988 | Fax: 520 621 9388 | |
| QY | Email: http://genome.arizona.edu | PCR Primers | |
| QY | FORWARD: gta aaa cga cgg tat cca gtg | FORWARD: | |
| QY | BACKWARD: gga aac agc tat gag cat g | BACKWARD: | |
| QY | Plate: 16 row: L column: 13 | Plate: | |
| QY | Seq primer: gta aaa cga cgg cca gtg. | Seq primer | |
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| ORIGIN | | | |
| QY | Query Match Score 29.9%; Best Local Similarity 73.0%; Pred. No. 2.4e-85; Matches 501; Conservative 0; Mismatches 184; Indels 1; Gaps 1; | Match | |
| QY | 193 GAGAGGAAATAGTTACTAGAGGAGTCCCGTGCTGATAGTGGCCATCTCAAGGGT 251 | Match | |
| Db | 127 GATTAATGAGATAACTGTAGAGGGACTCTTGTGCACTATCGAACCTCCGCAAGATGC 186 | Match | |
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| QY | 312 ATTATAAGGAAGAGTCAGGTCCAACATCCAGTACTCTACATGCTTCTCACTAC 371 | Match | |
| Db | 247 GTCATCAGAAGGCCATCGCAAGAACATCGAGTCAGTGGCTTGTGCACT 306 | Match | |
| QY | 372 AGGGCATGGACCAAAACTCGACGACAAATTGCGATACATCGATCAGCGAACCT 431 | Match | |
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| QY | Oryza sativa (japonica cultivar-group) | ORGANISM Oryza sativa | KEYWORDS |
| QY | EST. EST 16-OCT-2002 | REFERENCE | |
| QY | 1 (bases 1 to 705) | AUTHORS | |
| QY | Unneberg, P., Blalero, R.R., Jansson, S. and Sterky, F. | JOURNAL Unpublished (2002) | TITLE |
| QY | The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries | COMMENT | |
| QY | Unpublished (2002) | CONTACT: BHALERAO RUPALI R. | |
| QY | Umea Plant Science Center | Department of Plant Physiology | |
| QY | University of Umea, 901 87 Umea, Sweden | Tel: +46 90 786 5279 | |
| QY | Fax: +46 90 786 6676 | Email: rupali.bhalerao@plantphys.umu.se. | |
| FEATURES source | location/Qualifiers | | |
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| QY | 185 ATGACCAAGAGCGGAATAGTACTAGCGGTTAGCCATCGGTGTGCT 243 | Match | |

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| LOCUS | BG451848 | 667 bp | mRNA | linear | EST 16-MAR-2001 | Oy | 672 AGGATTGGCAGCACAGCAAGAAATGGATGGGATTCTCTTTAAGGAGGAAA |
| DEFINITION | NP_101C01DTR1002 Drought Medicago truncatula cDNA clone NF101C01DT | | | | | Db | 549 CGGATTGGCGAGGGATCGGAGAAGATGGATGGAAATGTCGTTCAGGA-AATTA |
| ACCESSION | BG451848 | 5' | mRNA sequence. | | | | 607 |
| VERSION | BG451848.1 | GI:13370630 | | | | | |
| KEYWORDS | EST | | | | | | |
| SOURCE | Medicago truncatula (barrel medic) | | | | | | |
| ORGANISM | Medicago truncatula | | | | | | |
| COMMENT | | | | | | | |
| REFERENCE | 1 (bases 1 to 667) | | | | | | |
| AUTHORS | Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imran, J.T., Weller, J.W. and May, G.D. | | | | | | |
| TITLE | Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library | | | | | | |
| JOURNAL | Unpublished (2000) | | | | | | |
| CONTACT | Contact: May GD | | | | | | |
| PLANT | Biology Division | | | | | | |
| THE SAMUEL ROBERTS NOBLE FOUNDATION | | | | | | | |
| 2510 Sam Noble Parkway, Ardmore, OK 73402, USA | | | | | | | |
| TELEPHONE | 580 221 7391 | | | | | | |
| FAX | 580 221 7391 | | | | | | |
| EMAIL | gdmay@noble.org | | | | | | |
| INSERT LENGTH | 667 | Std Error: | 0.00 | | | | |
| PLATE | 101 | row: C | column: 01 | | | | |
| SEQ PRIMER | TCACACAGGAACAGCTATGAC. | | | | | | |
| FEATURES | | | | | | | |
| SOURCE | Location/Qualifiers | | | | | | |
| ORIGIN | 1 .. 667 | | | | | | |
| QUERY MATCH | Organism="Medicago truncatula" | | | | | | |
| BEST LOCAL SIMILARITY | 26.9% | Score | 341.4; | DB 12; | Length | 667; | |
| MATCHES | 78.1%; | Pred. | No. 1.6e-75; | | | | |
| | 422; | Conservative | 0; | Mismatches | 117; | Indels | 1; |
| | | | | | | Gaps | 1; |
| OY | 252 | AATGTTCCCTCTAAAGTGTAGTAGGAAAGCTGGAGCTCTGGATGAGAACTGCAAGAACG | 311 | | | | |
| DB | 129 | AGTAGTCTCCAAAGTGTAGTCGAAGTGAAGTCTCTCAATGAGAGGTACAAACAA | 188 | | | | |
| QY | 312 | ATTTAAAGGAAAGTCACTGGTCCAAACCATCCAGTACTCTACATGCTTGTCACTAC | 371 | | | | |
| DB | 189 | ATTTAAAGGAAAGCTGTCAAGAACCTTCCAGTATCAATGCTTCTTCATAC | 248 | | | | |
| QY | 372 | AGGACATGCCAAAAACTCGCAGCACAAATTGAGGATACATGCATGAGCGCAACT | 431 | | | | |
| DB | 249 | AGGACATGCTGAGAACGGAGCACAAATTGAGGATACATGCAGGAGCAAGCA | 308 | | | | |
| QY | 432 | ATCGAATGCTGTCTGGAAAGAACAAAGAACATGGCGGTATTGCCATGGGTCT | 491 | | | | |
| DB | 309 | ACTGAGATGTTAAATGGAGAGAGAGAAATGACTGGCTGGGATTGAGGAA | 368 | | | | |
| QY | 492 | AGCATGAGCTGTGTGAGGAGGAGCATGGTGCGTGAAGCTGGGATTAGGAT | 551 | | | | |
| DB | 369 | AGCATGAGAAAGGGGGAGGAGCATGGTGCGTGAAGCTGGGATTAGGATAGGAG | 428 | | | | |
| FEATURES | source | | | | | | |
| ORIGIN | 1 .. 493 | | | | | | |
| QUERY MATCH | Organism="Populus alba x Populus tremula" | | | | | | |
| BEST LOCAL SIMILARITY | 26.3% | Score | 333.4; | DB 14; | Length | 493; | |
| MATCHES | 79.3%; | Pred. | No. 1.7e-73; | | | | |
| | 391; | Conservative | 0; | Mismatches | 102; | Indels | 0; |
| | | | | | | Gaps | 0; |
| OY | 477 | GCCATCGGTGTCGATGAGTCGTCGAGCTGGCTGTGCGTGTGAGTGGAA | 536 | | | | |
| DB | 1 | GCTCTGGTTTCAGATGAGGCTGGCTGAGCTGGCTGTGAGTGGAGTGGAA | 60 | | | | |

| | | | |
|----|-----|---|-----|
| QY | 537 | TTAGCTTATGGAAAGAAGAACTTTCTTCCCAATGTTCCACCATGGCAGACTG | 596 |
| Db | 61 | TTAGCTTATGGAAAGAAGAACTTTCTTCCCAATGTTCCACCATGGCAGATATA | 120 |
| QY | 597 | TTATGAGGTGCAAGTTATGGTTGATGAAACAAAGGAGGAAAGCTGGCAGTGAT | 656 |
| Db | 121 | ATATATGAGTCGAGCTNATGGATTGATGAAGTCAGAGAACGGAGACTCGTGGAT | 180 |
| QY | 657 | ATGACTGAGGAGGAGGATGGTGCAGCACAGAGAAATGGATGGGATTCCTT | 716 |
| Db | 181 | ATGACTGAGGAGGAGGATGGTGCAGCACAGAGAAATGGATGGAAATTCTCTA | 240 |
| QY | 717 | TTCAGGAGGAGAACTGGGAGGCCATGCAACAGTATGGAATGGCATAGGATACATG | 776 |
| Db | 241 | TTCAGGAGGAGAAACTGGGAGGCTATGAGCANTATGAAATGGCAATTGCAATTG | 300 |
| QY | 777 | GSGAGCGATTATGTTTCACTGGAACTTACCGGATATGGCTTACAGTAA | 836 |
| Db | 301 | GGTGACGACTTTAATGTTTCACTGGAACTTACCGGATATGGCTTACAGTAA | 360 |
| QY | 837 | AACCAGTCACCTTAACATAGAGCTTCCCTCATCAAACATAACGATACGTGAGCA | 896 |
| Db | 361 | AATCCATGTCATCTTAACATGGGCTTGTCTGATCAAGCTTGAGCCTATGAGGCC | 420 |
| QY | 897 | ATGGTCACTGCACATGGTGCAGAGAAAACCCAAAGCACGTTGAGA | 956 |
| Db | 421 | ATTCACAAATGCACTGTTATGGTAGANGAAGAACATCTAAGGTTGTCAGA | 480 |
| QY | 957 | AGAGGAAGCAA | 969 |
| Db | 481 | ANAGGAAAGCCA | 493 |

Search completed: July 7, 2004, 20:20:23
 Job time : 5096 secs